

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
Merberg, David
Treacy, Maurice
Spaulding, Vikki

(ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM

(iii) NUMBER OF SEQUENCES: 219

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: U.S.A.
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sprunger, Suzanne A.
(B) REGISTRATION NUMBER: 41,323

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTTT	TACAGACTTC	ACAGAGAATG	CAGTTGTCTT	GACTTCAGGT	CTGTCTGTTC	60
TGTTGGCAAG	TAAATGCAGT	ACTGTTCTGA	TCCCGCTGCT	ATTAGAATGC	ATTGTGAAAC	120
GA CTGGAGTA	TGATTA AAAAG	TTGTGTTCCC	CAATGCTTGG	AGTAGTGATT	GTTGAAGGAA	180
AAAATCCAGC	TGAGTGATAA	AGGCTGAGTG	TTGAGGAAAT	TTCTGCAGTT	TTAAGCAGTC	240
GTATTTGTGA	TTGAAGCTGA	GTACATTTTG	CTGGTGTATT	TTTAGGTAAA	ATGCTTTTTG	300
TTCATTTCTG	GTGGTGGGAG	GGGACTGAAG	CCTTTAGTCT	TTCCAGATG	CAACCTTAAA	360
ATCAGTGACA	AGAAACATTC	CAAACAAGCA	ACAGTCTTCA	AGAAATTAAA	CTGGCAAGTG	420
GAAATGTTTA	AACAGTTCAG	TGATCTTTAG	TGCATTGTTT	ATGTGTGGGT	TTCTCTCTCC	480
CCTCCCTTGG	TCTTAATTCT	TACATGCAGG	AACACTCAGC	AGACACACGT	ATGCGAAGGG	540
CCAGAGAAGC	CAGACCCAGT	AAGAAAAAAT	AGCCTATTTA	CTTTAAATAA	ACCAAACATT	600
CCATTTTAAA	TGTGGGGATT	GGGAACCACT	AGTTCTTTCA	GATGGTATTC	TTCAGACTAT	660
AGAAGGAGCT	TCCAGTTGAA	TTCACCAGTG	GACAAAATGA	GGAAAACAGG	TGAACAAGCT	720
TTTTCTGTAT	TTACATACAA	AGTCAGATCA	GTTATGGGAC	AATAGTATTG	AATAGATTTT	780
AGCTTTATGC	TGGAGTAACT	GGCATGTGAG	CAAAGTGTGT	TGGCGTGGGG	GTGGAGGGGT	840
GAGGTGGGCG	CTAAGCTTTT	TTTAAGATTT	TTCAGGTACC	CTTCACTAAA	GGCACCGAAG	900
GCTTAAAGTA	GGACAACCAT	GGAGCTTCCT	GTGGCAGGAG	AGACAACAAA	GCGCTATTAT	960
CCTAAGGTCA	AGAGAAGTGT	CAGCCTCACC	TGATTTTTAT	TAGTAATGAG	GA CTTGCCCTC	1020
AACTCCCTCT	TTCTGGAGTG	AAGCATCCGA	AGGAATGCTT	GAAGTACCCC	TGGGCTTCTC	1080
TTAACATTTA	AGCAAGCTGT	TTTTATAGCA	GCTCTTAATA	ATAAAGCCCA	AATCTCAAGC	1140
GGTGCTTGAA	GGGGAGGGAA	AGGGGGAAAAG	CGGGCAACCA	CTTTTCCCTA	GCTTTTCCAG	1200
AAGCCTGTTA	AAAGCAAGGT	CTCCCCACAA	GCAACTTCTC	TGCCACATCG	CCACCCCGTG	1260
CCTTTTGATC	TAGCACAGAC	CCTTCACCCC	TCACCTCGAT	GCAGCCAGTA	GCTTGATCC	1320
TTGTGGGCAT	GATCCATAAT	CGGTTTCAAG	GTAACGATGG	TGTCGAGKTC	TTTGGTGGGT	1380
TGAACTATGT	TAGAAAAGGC	CATTAATTTG	CCTGCAAATT	GTTAACAGAA	GGGTATTAAA	1440
ACCACAGCTA	AGTAGCTCTA	TTATAATACT	TATCCAGTGA	CTAAAACCAA	CTTAAAC ^a CAG	1500
TAAGTGGAGA	AATAACATGT	TCAAGAACTG	TAATGCTGGG	TGGGAACATG	TA ACTTG TAG	1560
ACTGGAGAAG	ATAGGCATTT	GAGTGGCTGA	GAGGGCTTTT	GGGTGGGAAT	GCAAAAATTC	1620

TCTGCTAAGA CTTTTTCAGG TGAACATAAC AGACTTGGCC AAGCTAGCAT CTTAGCGGAA 1680
 GCTGATCTCC AATGCTCTTC AGTAGGGTCA TGAAGGTTTT TCTTTTCCTG AGAAAACAAC 1740
 ACGTATTGTT TTCTCAGGTT TTGCTTTTTG GCCTTTTCT AGCTTAAAAA AAAAAAAAAA 1800

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Trp Val Ser Leu Ser Pro Pro Leu Val Leu Ile Leu Thr Cys Arg
 1 5 10 15
 Asn Thr Gln Gln Thr His Val Cys Glu Gly Pro Glu Lys Pro Asp Pro
 20 25 30
 Val Arg Lys Asn Ser Leu Phe Thr Leu Asn Lys Pro Asn Ile Pro Phe
 35 40 45

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1063 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAAGTTCCAT CTCTAGAACT GATTTTTATC CGTTCGTGTTT TTCAGGTCTT ATCTGTGTTA 60
 GTTGTGTGTT ACTATCAGGA GGCCCCCTTT GGACCCAGTG GATACAGATT ACGACTCTTC 120
 TTTTATGGTG TATGCAATGT CATTTCTATC ACTTGTGCTT ATACATCATT TTCAATAGTT 180
 CCTCCCAGCA ATGGGACCAC TATGTGGAGA GCCACAATA CAGTCTTCAG TGCCATTTTG 240
 GCTTTTTTAC TCGTAGATGA GAAAATGGCT TATGTTGACA TGGCTACAGT TGTTTGCAGC 300
 ATCTTAGGTG TTTGTCTTGT CATGATCCCA AACATTGTTG ATGAAGACAA TTCTTTGTTA 360

AATGCCTGGA AAGAAGCCTT TGGGTACACC ATGACTGTGA TGGCTGGACT GACCACTGCT 420
 CTCTCAATGA TAGTATACAG ATCCATCAAG GAGAAGATCA GCATGTGGAC TGCACTGTTT 480
 ACTTTTGGTT GGA CTGGGAC AATT TGGGGA ATATCTACTA TGTTTATTCT TCAAGAACCC 540
 ATCATCCCAT TAGATGGAGA AACCTGGAGT TATCTCATTG CTATATGTGT CTGTTCTACT 600
 GCAGCATTCT TAGGAGTTTA TTATGCCTTG GACAAATTCC ATCCAGCTTT GGT TAGCACA 660
 GTACAACATT TGGAGATTGT GGTAGCTATG GTCTTG CAGC TTCTCGTGCT GCACATATTT 720
 CCTAGCATCT ATGATGTTTT TGGAGGGGTA ATCATTATGA TTAGTGTTTT TGTCCTTGCT 780
 GGCTATAAAC TTTACTGGAG GAATTTAAGA AGGCAGGACT ACCAGGAAAT ATTAGACTCT 840
 CCCATTAAAT GAATACCTGA TTATTATTGT CTCATTAATG TTCAGTTATT AATATGTATA 900
 CTGCCATTTT AATGTTTACC TATGAATGTC TTTTG TGTTA TATAACTGAC AGAGTGCTAT 960
 AAAATATATA ATATATACAA ATGCAGAAAA TTTATTCTAG TCTAATATAT TCAAATACAA 1020
 ATATTAAATA TATGAAATAC GTTAAAAAAA AAAAAAAAAA AAA 1063

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Trp Arg Ala Thr Thr Thr Val Phe Ser Ala Ile Leu Ala Phe Leu
 1 5 10 15
 Leu Val Asp Glu Lys Met Ala Tyr Val Asp Met Ala Thr Val Val Cys
 20 25 30
 Ser Ile Leu Gly Val Cys Leu Val Met Ile Pro Asn Ile Val Asp Glu
 35 40 45
 Asp Asn Ser Leu Leu Asn Ala Trp Lys Glu Ala Phe Gly Tyr Thr Met
 50 55 60
 Thr Val Met Ala Gly Leu Thr Thr Ala Leu Ser Met Ile Val Tyr Arg
 65 70 75 80
 Ser Ile Lys Glu Lys Ile Ser Met Trp Thr Ala Leu Phe Thr Phe Gly
 85 90 95
 Trp Thr Gly Thr Ile Trp Gly Ile Ser Thr Met Phe Ile Leu Gln Glu

100	105	110
Pro Ile Ile Pro Leu Asp Gly Glu Thr Trp Ser Tyr Leu Ile Ala Ile		
115	120	125
Cys Val Cys Ser Thr Ala Ala Phe Leu Gly Val Tyr Tyr Ala Leu Asp		
130	135	140
Lys Phe His Pro Ala Leu Val Ser Thr Val Gln His Leu Glu Ile Val		
145	150	155
Val Ala Met Val Leu Gln Leu Leu Val Leu His Ile Phe Pro Ser Ile		
165	170	175
Tyr Asp Val Phe Gly Gly Val Ile Ile Met Ile Ser Val Phe Val Leu		
180	185	190
Ala Gly Tyr Lys Leu Tyr Trp Arg Asn Leu Arg Arg Gln Asp Tyr Gln		
195	200	205
Glu Ile Leu Asp Ser Pro Ile Lys		
210	215	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGGCCAAAGA GGCCTAGCCG GGAGCGGGCG AGGCGGCGGC GGCAGCAGCG ATGGCAGGAA	60
TAGAGTTGGA GCGGTGCCAG CAGCAGGCCA ACGAGGTGAC GGAAATTATG CGTAACAACT	120
TCGGCAAGGT CCTGGAGCGT GGTGTGAAGC TGGCCGAAC TCGAGCAGCGT TCAGACCAAC	180
TCCTGGATAT GAGCTCAACC TTCAACAAGA CTACACAGAA CCTGGCCCAG AAGAAGTGCT	240
GGGAGAACAT CCGTTACCGG ATCTGCGTGG GGCTGGTGGT GGTGGTGTC CTGCTCATCA	300
TCCTGATTGT GCTGCTGGTC GTCTTTCTCC CTCAGAGCAG TGACAGCAGT AGTGCC	356

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Gly Ile Glu Leu Glu Arg Cys Gln Gln Gln Ala Asn Glu Val
1 5 10 15
Thr Glu Ile Met Arg Asn Asn Phe Gly Lys Val Leu Glu Arg Gly Val
20 25 30
Lys Leu Ala Glu Leu Gln Gln Arg Ser Asp Gln Leu Leu Asp Met Ser
35 40 45
Ser Thr Phe Asn Lys Thr Thr Gln Asn Leu Ala Gln Lys Lys Cys Trp
50 55 60
Glu Asn Ile Arg Tyr Arg Ile Cys Val Gly Leu Val Val Val Gly Val
65 70 75 80
Leu Leu Ile Ile Leu Ile Val Leu Leu Val Val Phe Leu Pro Gln Ser
85 90 95
Ser Asp Ser Ser Ser Ala
100

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 92

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGCCTCAAC TTTGGCGTCG TGAGATTCTT GTGAGGCGTC TGCCTGGAAG CCGGCAGCAA	60
TTTTGCTTCT TTAAAGAGAA AAAGAAGGCT AGGGACTCAG ATTCCTGGAT TCTGAGATCC	120
AGACCAGCTC CTCCCAGACC TCTCCAGAAG AAGCCATGGG AACCCCTCGT ATCCAGCATT	180
TGCTGATCCT CCTGGTCCTA GGAGCCTCCC TCCTGACCTC GGGCCTAGAG CTGTATTGTC	240
AAAAGGGTCT GTCCATGACT GTGGAAGCAG ATCCAGCCAA TATGTTTAAC TGGACCACAG	300
AGGAAGTGGA GACTTGTGAC AAAGGGGCAC TTTGCCAGGA AACCATACTA ATAATTAAAG	360
CAGGGACTGA GACAGCCATT TTGGCCACGA AGGGCTGCAT CCCGGAAGGG GAGGAGGCCA	420
TAACAATTGT CCAGCACTCT TCACCTCCCG GCCTGATCGT GACCTCCTAC AGTAACTACT	480
GTGAGGATTC CTTCTGTAAT GACAAAGACA GCCTGTCTCA GTTTTGGGAG TTCAGTGAGA	540
CCACAGCTTC CACTGTGTCA ACAACCCTCC ATTGTCCAAC CTGTGTGGCT TTGGGGACCT	600
GTTTCAGTGC TCCTTCTCTT CCCTGTCCCA ATGGTACAAC TCGATGCTAT CAAGGAAAAC	660
TTGAGATCAC TGGAGGTGGC ATTGAGTCGT CTGTGGAGGT CAAAGGCTGT ACAGCCATGA	720
TTGGCTGCAG GCTGATGTCT GGAATCTTAG CAGTAGGACC CATGTTTGTG AGGGAAGCGT	780
GCCCACATCA GCTGCTCACT CAACCTCGAA AGACTGAAAA TGGGGCCACC TGTCTTCCCA	840
TTCTGTTTTG GGGGTTACAG CTACTGCTGC CATTGCTGCT GCCATCATTT ATTCAC'TTTT	900
CCTAAGAAGG CACTTCTGGG CCTGGGTCTG AGGACATCTT TTTTGA'CTGG GAGCCTTCTT	960
ACTGTTGAGG TTCAACAAGC TGAGGAGTAG ATGGGAATTT GAGGGAGAAT ACAGAGATAC	1020
TATGAACGTA TTTGACATTT TTAATACAAT TTCTGCTATA ATTTTGTAT GCAGTAGGCG	1080
TTACTAATAA ACATTTCTGC TGTGAAAAAA AAAAAAAAAA AAAAAAAAAA A	1131

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Gly	Thr	Pro	Arg	Ile	Gln	His	Leu	Leu	Ile	Leu	Leu	Val	Leu	Gly
1								5			10			15	

Ala Ser Leu Leu Thr Ser Gly Leu Glu Leu Tyr Cys Gln Lys Gly Leu
20 25 30

Ser Met Thr Val Glu Ala Asp Pro Ala Asn Met Phe Asn Trp Thr Thr
35 40 45

Glu Glu Val Glu Thr Cys Asp Lys Gly Ala Leu Cys Gln Glu Thr Ile
50 55 60

Leu Ile Ile Lys Ala Gly Thr Glu Thr Ala Ile Leu Ala Thr Lys Gly
65 70 75 80

Cys Ile Pro Glu Gly Glu Glu Ala Ile Thr Ile Val Gln His Ser Ser
85 90 95

Pro Pro Gly Leu Ile Val Thr Ser Tyr Ser Asn Tyr Cys Glu Asp Ser
100 105 110

Phe Cys Asn Asp Lys Asp Ser Leu Ser Gln Phe Trp Glu Phe Ser Glu
115 120 125

Thr Thr Ala Ser Thr Val Ser Thr Thr Leu His Cys Pro Thr Cys Val
130 135 140

Ala Leu Gly Thr Cys Phe Ser Ala Pro Ser Leu Pro Cys Pro Asn Gly
145 150 155 160

Thr Thr Arg Cys Tyr Gln Gly Lys Leu Glu Ile Thr Gly Gly Gly Ile
165 170 175

Glu Ser Ser Val Glu Val Lys Gly Cys Thr Ala Met Ile Gly Cys Arg
180 185 190

Leu Met Ser Gly Ile Leu Ala Val Gly Pro Met Phe Val Arg Glu Ala
195 200 205

Cys Pro His Gln Leu Leu Thr Gln Pro Arg Lys Thr Glu Asn Gly Ala
210 215 220

Thr Cys Leu Pro Ile Pro Val Trp Gly Leu Gln Leu Leu Leu Pro Leu
225 230 235 240

Leu Leu Pro Ser Phe Ile His Phe Ser
245

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTCCGGGCC	GGCTGCGGAG	CGACTCCCCG	CCGCCAAGTG	GGCGGCGTGG	CTGTCGGGAA	60
AGAAGGGCTG	GGGCCTGCCG	TTCTTCCTCC	CGAGTATCCC	CTCCAGCTGG	ACGACCCAC	120
GCTGCAGCAC	GGGCTTCCGG	CTTCTCTCCT	CAGTGGCCAA	TTCGAGGGCA	CAGCGGGCTC	180
CGGAGGCGCG	GCGGCAAGCC	TATCCCGCCT	CCCAACCACA	GCCTCCAGCA	CCCGAGAGAA	240
CGGCCGCCCA	CAGCACACGT	TCTCCGACA	GGAGGGCGAA	GGCCAAGAC	CTGGAGAGAT	300
GGTCAGCTCT	CAAAAAAGGC	ACAAACAATT	GAAGGATGGA	TACCATGGCA	TATGTTAAAA	360
GCGTGTGAA	AGGAAAATAA	GAAAGCCAGG	AATCTCAGGA	TGAATCAGTC	TAGATCGAGA	420
TCAGATGGTG	GCAGTGAAGA	AACCTTACCT	CAAGACCATA	ATCATCATGA	AAATGAGAGA	480
AGATGGCAGC	AAGAGCGTCT	CCACAGAGAA	GAGGCCTATT	ATCAGTTTAT	TAATGAACTC	540
AATGATGAAG	ATTATCGGCT	TATGAGAGAC	CATAATCTTT	TAGGCACCCC	TGGAGAAATA	600
ACATCAGAAG	AACTGCAACA	GCGGTTAGAT	GGCGTCAAGG	AACAAC TAGC	ATCTCAGCCT	660
GACTTGAGAG	ATGGAACGAA	TTACAGAGAC	TCAGAAGTCC	CTAGAGAAAG	TTCACATGAA	720
GATTCTCTTC	TAGAATGGTT	GAACACCTTT	CGGCGCACAG	GAAATGCAAC	TCGAAGTGGA	780
CAAAATGGGA	ACCAAAC TTG	GAGAGCTGTG	AGTCGAACAA	ACCCGAACAA	TGGAGAGTTT	840
CGGTTTAGTT	TGGAAATCCA	CGTAAATCAT	GAAAATAGAG	GATTTGAAAT	TCATGGAGAA	900
GATTATACAG	ACATTCCACT	TTCAGATAGT	AACAGAGATC	ATACTGCAAA	TAGGCAACAA	960
AGGTCAACTA	GTCCTGTGGC	TAGGCGAACA	AGAAGCCAAA	CCTCAGTGAA	TTTCAATGGT	1020
AGTAGTTCCA	ACATTCCAAG	GACTAGGCTT	GCTTCAAGGG	GGCAAAATCC	AGCTGAAGGA	1080
TCTTTCTCAA	CATTGGGAAG	GTTAAGAAAT	GGAATTGGGG	GAGCAGCTGG	CATTCTCTGA	1140
GCTAACGCTT	CACGCACTAA	TTTCAGTAGT	CACACAAACC	AATCAGGTGG	TAGTGAAC TC	1200
AGGCAAAGGG	AGGGGCAACG	GTTTGGAGCA	GCACATGTTT	GGGAAAATGG	GGCTAGAAGT	1260
AATGTTACAG	TGAGGAATAC	AAACCAAAGA	TTAGAGCCAA	TAAGATTACG	ATCTACTTCC	1320
AATAGTCGAA	GCCGTTCAAC	AATTCAGAGA	CAGAGTGGCA	CTGTTTATCA	TAATTCCCAA	1380
AGGGAAAGTA	GACCAGTACA	GCAAACCACT	AGAAGATCTG	TTAGGAGGAG	AGGTAGA ACT	1440
CGAGTCTTTT	TAGAGCAAGA	TAGAGAACGA	GAACGCAGAG	G TACTGCATA	TACCCCATTC	1500
TCTAATTCAA	GGCTTGTGTC	AAGAATAACA	G TAGAAGAAG	GAGAAGAATC	CAGCAGATCC	1560
TCAACTGCTG	TACGACGACA	TCCAACAATC	ACACTGGACC	TTCAAGTGAG	AAGGATCCGT	1620

CCTGGAGAAA ATAGAGATCG GGATAGTATT GCAAATAGAA CTCGATCCAG AGTAGGGCTA 1680
GCAGAAAATA CAGTCACTAT TGAAAGCAAT AGTGGGGGCT TTCGCCGAAC CATTCTCTCGT 1740
TTAGAGCGGT CAGGTATTCG AACCTATGTT AGTACCATAA CAGTTCCCCT TCGTAGGATT 1800
TCTGAGAATG AGCTTGTTGA GCCATCATCA GTGGCTCTTC GGTCAATTTT AAGGCAGATC 1860
ATGACTGGGT TTGGAGAACT GAGTTCTCTA ATGGAGGCCG ATTCTGAGTC AGAACTTCAA 1920
AGAAATGGCC AGCATTTACC AGACATGCAC TCAGAACTGA GTAACCTAGG TACAGATAAC 1980
AACAGGAGCC AGCACAGGGA AGGTCCTCT CAAGACAGGC AGGCCCAAGG AGACAGCACT 2040
GAAATGCATG GTGAAAACGA GACCACCCAG CCTCATACTC GAAACAGTGA CAGTAGGGGT 2100
GGCAGGCAGT TGCGAAATCC AAACAATTTA GTTGAAACTG GAACACTACC CATTCTTCGC 2160
CTTGCTCACT TTTTTTTACT AAATGAAAGT GATGATGATG ATCGAATACG TGGTTTAACC 2220
AAAGAGCAGA TTGACAATCT TTCCACCAGG CACTATGAGC ATAACAGTAT TGATAGTGAA 2280
CTAGGTAAAA TCTGTAGTGT TTGTATTAGT GACTATGTAA CTGGAAACAA GCTCAGGCAA 2340
TTACCTTGCA TGCATGAATT TCACATTCAT TGTATTGACC GATGGCTCTC AGAGAATTGC 2400
ACTTGTCCGA TCTGTCGGCA GCCTGTTTTA GGGTCTAACA TAGCAAACAA TGGGTAAGGT 2460
GATGGGATCT ACTCAAATAC TGTTTTTTAG TAGAACTGAA TGTTCAAGCA TTGTTTTGCT 2520
GAGTTATTTG TGATTAGCTA ACCAGGATGA AAAATAACAG ATTATATATA GTTTGAACTA 2580
TTTTTCGTGT GCTTTTTTAA ACTTGTTAAA AAGAAATTTA TATAAAATTT AAAATACAAA 2640
TGTTAAATTA TCCAGAAATA CAGAATAGTT AATATTGCTA GAACCAAATA ACCTCTAAAA 2700
TGTTTTTATT TTGGTAATTT TGTCATGCTA AGCACTTTTG TATCTGCACA ATTCAGTAGG 2760
TTAAGAATCA ATCTTCTTTT TCTTAATAGT ACAGCAGACT TTAGCTTCAA GTTTCATAGG 2820
CTTAGTACTT ATATCTAGAC ATTTGTGTCT AAATAAGCTT TTCATTAACT TTTTATTTTA 2880
AGGACAGTAT CTTTTCATGA AAGAGTATTT GGCTGAATGT TTGCTATATA TATGTTACTT 2940
GAAATGTTAA ATTTAATATG CAGCATACCA TAGGTGTATA TATAGGTATA TAATTTTAAG 3000
GTTAAAATAT TCAGTCTAAC AAGTTTGGTT CTTATTTAAG CTTTGGGCT AATACTGCAT 3060
ATGGCACAAAT GTTTAATATT GGCAAGTTCA TCTCAGAGAA AGGGGATTCA GATATAATTT 3120
TAAAGTAGAG ATAATTTACT GAAGCGTCTC TGACAATCTA ACTTATTAGA CAGCAAGCAA 3180
TATATAATAC TGAAAAAGTA TTCAGAAATG GAAAATTTAC ATCATATAGG TTATTTAACT 3240
TGTGTTCAGC CTTTTTGTA CTTTTTGAA AGTGCAAACA ATTCTTTGGA TTATTAAATA 3300

AGGTATACAG TATGCATGGT TTCTCAAATT TAGCTTTAAA ATCTAAAAGT CTATAAAGAA 3360
 TCAGATGCAT AGGCAATATG TTAAGTTCAC TTGGAGGCTA AAAATCTCCA GTGAAAACAA 3420
 AACGAAAACC TTTAAGAGAA TGTAGAGTTT ATATAAACAC AAAGTATGCA TTGAAGATCT 3480
 GTTTCTACCA ATAAACATTA AAACAAAAAA AAAAAAAAAA AAAAAAA 3527

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 685 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Gln Ser Arg Ser Arg Ser Asp Gly Gly Ser Glu Glu Thr Leu
 1 5 10 15
 Pro Gln Asp His Asn His His Glu Asn Glu Arg Arg Trp Gln Gln Glu
 20 25 30
 Arg Leu His Arg Glu Glu Ala Tyr Tyr Gln Phe Ile Asn Glu Leu Asn
 35 40 45
 Asp Glu Asp Tyr Arg Leu Met Arg Asp His Asn Leu Leu Gly Thr Pro
 50 55 60
 Gly Glu Ile Thr Ser Glu Glu Leu Gln Gln Arg Leu Asp Gly Val Lys
 65 70 75 80
 Glu Gln Leu Ala Ser Gln Pro Asp Leu Arg Asp Gly Thr Asn Tyr Arg
 85 90 95
 Asp Ser Glu Val Pro Arg Glu Ser Ser His Glu Asp Ser Leu Leu Glu
 100 105 110
 Trp Leu Asn Thr Phe Arg Arg Thr Gly Asn Ala Thr Arg Ser Gly Gln
 115 120 125
 Asn Gly Asn Gln Thr Trp Arg Ala Val Ser Arg Thr Asn Pro Asn Asn
 130 135 140
 Gly Glu Phe Arg Phe Ser Leu Glu Ile His Val Asn His Glu Asn Arg
 145 150 155 160
 Gly Phe Glu Ile His Gly Glu Asp Tyr Thr Asp Ile Pro Leu Ser Asp
 165 170 175
 Ser Asn Arg Asp His Thr Ala Asn Arg Gln Gln Arg Ser Thr Ser Pro
 180 185 190

Val Ala Arg Arg Thr Arg Ser Gln Thr Ser Val Asn Phe Asn Gly Ser
195 200 205

Ser Ser Asn Ile Pro Arg Thr Arg Leu Ala Ser Arg Gly Gln Asn Pro
210 215 220

Ala Glu Gly Ser Phe Ser Thr Leu Gly Arg Leu Arg Asn Gly Ile Gly
225 230 235 240

Gly Ala Ala Gly Ile Pro Arg Ala Asn Ala Ser Arg Thr Asn Phe Ser
245 250 255

Ser His Thr Asn Gln Ser Gly Gly Ser Glu Leu Arg Gln Arg Glu Gly
260 265 270

Gln Arg Phe Gly Ala Ala His Val Trp Glu Asn Gly Ala Arg Ser Asn
275 280 285

Val Thr Val Arg Asn Thr Asn Gln Arg Leu Glu Pro Ile Arg Leu Arg
290 295 300

Ser Thr Ser Asn Ser Arg Ser Arg Ser Pro Ile Gln Arg Gln Ser Gly
305 310 315 320

Thr Val Tyr His Asn Ser Gln Arg Glu Ser Arg Pro Val Gln Gln Thr
325 330 335

Thr Arg Arg Ser Val Arg Arg Arg Gly Arg Thr Arg Val Phe Leu Glu
340 345 350

Gln Asp Arg Glu Arg Glu Arg Arg Gly Thr Ala Tyr Thr Pro Phe Ser
355 360 365

Asn Ser Arg Leu Val Ser Arg Ile Thr Val Glu Glu Gly Glu Glu Ser
370 375 380

Ser Arg Ser Ser Thr Ala Val Arg Arg His Pro Thr Ile Thr Leu Asp
385 390 395 400

Leu Gln Val Arg Arg Ile Arg Pro Gly Glu Asn Arg Asp Arg Asp Ser
405 410 415

Ile Ala Asn Arg Thr Arg Ser Arg Val Gly Leu Ala Glu Asn Thr Val
420 425 430

Thr Ile Glu Ser Asn Ser Gly Gly Phe Arg Arg Thr Ile Ser Arg Leu
435 440 445

Glu Arg Ser Gly Ile Arg Thr Tyr Val Ser Thr Ile Thr Val Pro Leu
450 455 460

Arg Arg Ile Ser Glu Asn Glu Leu Val Glu Pro Ser Ser Val Ala Leu
465 470 475 480

Arg Ser Ile Leu Arg Gln Ile Met Thr Gly Phe Gly Glu Leu Ser Ser
485 490 495

Leu Met Glu Ala Asp Ser Glu Ser Glu Leu Gln Arg Asn Gly Gln His
500 505 510

Leu Pro Asp Met His Ser Glu Leu Ser Asn Leu Gly Thr Asp Asn Asn
515 520 525

Arg Ser Gln His Arg Glu Gly Ser Ser Gln Asp Arg Gln Ala Gln Gly
530 535 540

Asp Ser Thr Glu Met His Gly Glu Asn Glu Thr Thr Gln Pro His Thr
545 550 555 560

Arg Asn Ser Asp Ser Arg Gly Gly Arg Gln Leu Arg Asn Pro Asn Asn
565 570 575

Leu Val Glu Thr Gly Thr Leu Pro Ile Leu Arg Leu Ala His Phe Phe
580 585 590

Leu Leu Asn Glu Ser Asp Asp Asp Arg Ile Arg Gly Leu Thr Lys
595 600 605

Glu Gln Ile Asp Asn Leu Ser Thr Arg His Tyr Glu His Asn Ser Ile
610 615 620

Asp Ser Glu Leu Gly Lys Ile Cys Ser Val Cys Ile Ser Asp Tyr Val
625 630 635 640

Thr Gly Asn Lys Leu Arg Gln Leu Pro Cys Met His Glu Phe His Ile
645 650 655

His Cys Ile Asp Arg Trp Leu Ser Glu Asn Cys Thr Cys Pro Ile Cys
660 665 670

Arg Gln Pro Val Leu Gly Ser Asn Ile Ala Asn Asn Gly
675 680 685

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAGCCTGGGC TCCGCGCAGC CCACCGATCT GGGCGCCCAC AAGCGGCCGG CATCCGTGTC	60
GAGCAGCGCT GCCGTGGAGC ACGAGCAGCG TGAGGCGGCA GCCAAGGAGA AACAAACGCC	120
GCCGCCTGCG CACCGGGGCC CGGCCGACAG CCTGTCCACC GCGGCCGGGG CCGCCGAGCT	180

GAGCGCGGAA GGTGCGGGCA AGAGCCGCGG GTCTGGAGAG CAGGACTGGG TCAACAGGCC	240
CAAGACCGTG CGCGACACGC TGCTGGCGCT GCACCAGCAC GGCCACTCGG GGCCCTTCGA	300
GAGCAAGTTT AAGAAGGAGC CGGCCCTGAC TGCAGGCAGG TTGTTGGGTT TCGAGGCCAA	360
CGGGGCCAAC GGGTCTAAAG CAGTTGCAAG AACAGCAAGG AAAAGGAAGC CCTCTCCAGA	420
ACCAGAAGGT GAAGTCGGGC CCCCTAAGAT CAACGGAGAG GCCCAGCCGT GGCTGTCCAC	480
ATCCACAGAG GGGCTCAAGA TCCCCATGAC TCCTACATCC TCTTTTGTGT CTCCGCCACC	540
ACCCACTGCC TCACCTCAT TCCAACCGGAC CACACCGCCT GAAGCGGCCC AGAATGGCCA	600
GTCCCCCATG GCAGCCCTGA TCTTAGTAGC AGACAATGCA GGGGGCAGTC ATGCCTCAAA	660
AGATGCCAAC CAGGTTCACT CCACTACCAG GAGGAATAGC AACAGTCCGC CCTCTCCGTC	720
CTCTATGAAC CAAAGAAGGC TGGGCCCCAG AGAGGTGGGG GGCCAGGGAG CAGGCAACAC	780
AGGAGGACTG GAGCCAGTGC ACCCTGCCAG CCTCCCGGAC TCCTCTCTGG CAACCAGTGC	840
CCCCTGTGTC TGCACCTCT GCCACGAGCG GCTGGAGGAC ACCCATTTTG TGCAGTGCCC	900
GTCCGTCCCT TCGCACAAGT TCTGCTTCCC TTGCTCCAGA CAAAGCATCA AACAGCAGGG	960
AGCTAGTGGA GAGGTCTATT GTCCCAGTGG GGAAAAATGC CCTCTTGTGG GCTCCAATGT	1020
CCCCTGGGCC TTTATGCAAG GGGAAATTGC AACCATCCTT GCTGGAGATG TGAAAGTGAA	1080
AAAAGAGAGA GACTCGTGAC TTTTCCGGTT TCAGAAAAAC CCAATGATTA CCCTTAATTA	1140
AAACTGCTTG AATTGTATAT ATATCTCCAT ATATATATAT ATCCAAGACA AGGGAAATGT	1200
AGACTTCATA AACATGGCTG TATAATTTTG ATTTTTTTTG AATACATTGT GTTTCTATAT	1260
TTTTTTTGAC GACAAAAGGT ATGTACTTAT AAAGACATTT TTTTCTTTTG TTAACGTTAT	1320
TAGCATATCT TTGTGCTTTA TTATCCTGGT GACAGTTACC GTTCTATGTA GGCTGTGACT	1380
TGCGCTGCTT TTTTAGAGCA CTTGGCAAAT CAGAAATGCT TCTAGCTGTA TTTGTATGCA	1440
CTTATTTTAA AAAAAAAAAA AAA	1463

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Thr	Pro	Thr	Ser	Ser	Phe	Val	Ser	Pro	Pro	Pro	Pro	Thr	Ala	Ser	1	5	10	15
Pro	His	Ser	Asn	Arg	Thr	Thr	Pro	Pro	Glu	Ala	Ala	Gln	Asn	Gly	Gln	20	25	30	
Ser	Pro	Met	Ala	Ala	Leu	Ile	Leu	Val	Ala	Asp	Asn	Ala	Gly	Gly	Ser	35	40	45	
His	Ala	Ser	Lys	Asp	Ala	Asn	Gln	Val	His	Ser	Thr	Thr	Arg	Arg	Asn	50	55	60	
Ser	Asn	Ser	Pro	Pro	Ser	Pro	Ser	Ser	Met	Asn	Gln	Arg	Arg	Leu	Gly	65	70	75	80
Pro	Arg	Glu	Val	Gly	Gly	Gln	Gly	Ala	Gly	Asn	Thr	Gly	Gly	Leu	Glu	85	90	95	
Pro	Val	His	Pro	Ala	Ser	Leu	Pro	Asp	Ser	Ser	Leu	Ala	Thr	Ser	Ala	100	105	110	
Pro	Leu	Cys	Cys	Thr	Leu	Cys	His	Glu	Arg	Leu	Glu	Asp	Thr	His	Phe	115	120	125	
Val	Gln	Cys	Pro	Ser	Val	Pro	Ser	His	Lys	Phe	Cys	Phe	Pro	Cys	Ser	130	135	140	
Arg	Gln	Ser	Ile	Lys	Gln	Gln	Gly	Ala	Ser	Gly	Glu	Val	Tyr	Cys	Pro	145	150	155	160
Ser	Gly	Glu	Lys	Cys	Pro	Leu	Val	Gly	Ser	Asn	Val	Pro	Trp	Ala	Phe	165	170	175	
Met	Gln	Gly	Glu	Ile	Ala	Thr	Ile	Leu	Ala	Gly	Asp	Val	Lys	Val	Lys	180	185	190	
Lys	Glu	Arg	Asp	Ser												195			

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CATTTTCTG	GTCCTTCTTA	AAAGTAATCA	CTCTTAAATT	TTGTGCTTAT	TCTGTTGTTT	60
TAAAAAATAG	TTTAAACAAA	TATGTGTGTA	CTCATAAACA	TAGGTACTT	TTGCTTCTTT	120
TTGAGATATA	TTTAAATTTT	ATTGTGGTCT	ACATATTCTT	CAGCAGTTTG	TTTTTTTACC	180
CAATATTATG	TTTCATCTGT	ATTACTGCAT	TTACTATCCC	TAGTTGATTC	ACTTCCCTGA	240
AGTACAATAT	TCAGTTGTGT	GGCTATACCA	TAATTTAGTT	ATTCATTTTG	TTGTCAGTAA	300
AATTTGGGTG	ATTATCAGAT	TTTTTTCTAG	CATGAAAAAT	GCTACTARGA	ACATTCSTGT	360
ATGTGTCTAA	TGGTATACAC	TTTCAAGTGT	TTTTTTATAT	ATGTGAGAGT	AGATTACTTG	420
GACCTTGAAG	ATGAACATGC	TATCTTTTCC	AGATACTGCC	AATTATTTCA	GCAAGATATG	480
AGTTCCCATC	ATTTTATATT	TGTCAGCATT	TGATATTTCC	AGGCCTAGTG	ATTTCCAGTC	540
ATTTACTGGA	TATAATATGA	TTATCTCTGT	AGGGAGTTGA	TTCCATCTC	CTCAATTACT	600
AATAAAGTTA	AAAATCTTTT	CATATGTTTT	ATTGCCATTT	TTATTTCTTC	TGTAAAGTAC	660
CTACTCATGG	CTTTTTCTCA	TTTTTTGTTT	GTCATCATTG	AATTATAGGA	GTTTTGAGAG	720
AGTGAGCAAG	CTAGTCTGTG	TGTGTGTGTG	TGTGCGTGTG	TGTGTATCTC	CTTAATGTGT	780
TATATGTGAT	TGGAACTTCT	TCTCCACCT	TGATGCTTCC	TTTCTTCCCC	ACTTGTTTTA	840
GGTATCTTCT	GATGAAGTGG	AGTTATTTAT	GGTATGTTCT	CAGGAGCTAC	AATTTTTAAT	900
TTCAATATAA	TCAGTGTTTT	TAATTATCTT	ATGTTTAGCT	CTTTTGGGTC	ATGCTTAGGA	960
AATTCCTTCT	AAATTTTATT	GATAACAGTC	TTCCATACTT	TCTTCTAAAG	TCTTATATTT	1020
TGGCCTTTCA	TATTTATTCC	TTTAATCCAM	CTGGAGTAGA	TTTTTTTTTTT	CCCTCTGTAG	1080
AGTTTGGAGT	AGAGATTTTA	TTTCCTTTTT	TTTTTTTTTTT	TTTTTTTCTT	TTTTTTTGAG	1140
ACAGAGTCTT	GCTCTGTCGC	CCAGGCTGGA	GTGCAGTGGC	ACTATCTCAG	CTCACTGCAA	1200
CCTCCACCTC	CTGGGTTCAG	GCGATTCTCC	TGCCTCCGCC	TCCCGAGTAG	CTGGGACTAC	1260
AGGCATGTGC	CACCACGCCC	AGCTAATTTT	TTGTATTTT	TTTAGTAGAG	ATGGGGTTCC	1320
ACCATGTTAG	CTAGGATGAT	TTGATTTTCC	TGACCTTGTG	ATCCGCCCCG	CTCGGCCTCC	1380
CAAAATGCTG	GGATTATAGG	TGTGAGCCAC	CACGTGGCCT	CATTTTATTC	TTTCATGTGG	1440
ATAGGCAGTT	GTTCCAGAAG	TATATAGTGA	GGAGCTTCTT	CTTTCTCTAA	TGATCTGCAA	1500
TGTCACCTTC	ATCATTTATG	AAGGTTGCAC	ATATACATGG	GAATTTTTTA	GTCTGGCATT	1560
AAATGTTCTT	CAAAAGAGTT	CCTGCAAACG	TTTTTGTTTT	TATTTCTTAC	TGTTCCCTTC	1620
ACGTACTCTC	TACTGAACTA	AACTCTGTAA	TGTGTCTCGA	AACTGTCCCA	CAATTTTCCT	1680

TGTCTTAAGA GTTTAATGCT TTCATACACC TCTCACATTC AGCCTTGTGC TATTGTCTTA 1740
 GGTATATTTA TTTCTCTTTT GCTCCCAATT ATGTTGTAAA CTTTGTGAAG CAGGAAGGAT 1800
 ATATTGTTCA TCTTTGGTAG CATTAAACAA TGAATACAGT GTTTTTTACT TAATAGATAT 1860
 TTGGTAAATC ATTGAACTAA ATTGGGGTTT GGAATTGAAG GTCTTAGAAA TTACCTGACC 1920
 ACTCCCATTA TATTTGCCCA TCCATGATCA CTGAGATTTA TAGAGATTAG ATGCAATGCC 1980
 CAGTTTCACA TATGTTTTTG CATCACTGTC TCTTTTTTTC TTGAGCTTAT TCCAGAGTGT 2040
 CTTTAAATAT CCATTCCATG ATCAAATGGC TGAACATTA AAATGCTGTC CAGAAGTGTA 2100
 AAGCAATATG AAGATGCTAG AAAAGTTGAA GAGACACATA TATGGTAGGT CCAAGACCAT 2160
 TACACTTACT GAGTCCATTA CTAAAAATGA TGTTCACTTA ACATCAAAAC ACTCAGGATT 2220
 ACCCAAGCAC AATATACTGA TTTGCACCTC TGCCTTTGTT CATGCCCTT GTTCAGGAGA 2280
 ACTGCTTTCA TGTGCTACTG TCCATAGATC TTCTCTATCC TTACAGATTA ATTTCTTCCT 2340
 TTTGAATGCT ATGTTTCCAT ACTTTGACAT TCCTTCTGCA CCATTCAGAC CATATTTTAG 2400
 TTCTTTTTTA TGGTATCTCT CACTTTTGAT TGTCACCCCT TAAGTCAAAG ACAATTTTTT 2460
 CATCTGTGTC TTCTCAACAC CCAGCACAGG GCTATGTTTG GTAAAAATTA GGTATCCAAG 2520
 ATGTACTAAA TGAAAAAAAA AAAAAAA 2547

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Phe	Phe	Lys	Arg	Val	Pro	Ala	Asn	Val	Phe	Val	Phe	Ile	Ser	Tyr
1				5					10					15	
Cys	Ser	Leu	His	Val	Leu	Ser	Thr	Glu	Leu	Asn	Ser	Val	Met	Cys	Leu
			20					25					30		
Glu	Thr	Val	Pro	Gln	Phe	Ser	Leu	Ser							
			35				40								

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCTCAACGGC CTCTTCTGGT TGCTGTCTTC CTCGTCCCTC CGGCCCTTCT TCCTACTCAG	60
CGTCTCACTT TTGGCCTATT TTCTGCTGGA TCTCTGGCAG CCTCGCTTTC TCCCTGACGT	120
TTCAGCATCA TCCCCAGAGG AGCCACACTC TGACAGTGAG GGTGCGGGGT CAGGCGCCCCG	180
GCCGCACCTG CTGAGTGTGC CCGAGTTGTG CAGATACCTG GCTGAGAGCT GGCTCACCTT	240
CCAGATTAC CTGCAGGAGC TGCTGCAGTA CAAGAGGCAG AATCCAGCTC AGTTCTGCGT	300
TCGARTCTGC TCTGGCTGTG CTGTGTTGGC TGTGTTGGGA CACTATGTTC CAGGGATTAT	360
GATTTCTTAC ATTGCTCTGT TGAGTATCCT GCTGTGGCCC CTGGTGGTTT ATCATGARCT	420
GATCCAGAGG ATGTWCACTC GCCTGGAGCC CCTGCTCATG CAGCTGGACT ACAGCATGAA	480
GGCAGAAKCC AATGCCCTGC ATCACAACA CGACAAGAGG AAGCGTCAGG GGAAGAATGC	540
ACCCCCAGGA GGTGATGAGC CACTGGCAGA GACAGAGAGT GAAAGCGAGG CAGAGCTGGC	600
TGGCTTCTCC CCAGTGGTGG ATGTGAAGAA AACAGCATTG GCCTTGGCCA TTACAGACTC	660
AGAGCTGTCA GATGAGGAGG CTTCTATCTT GGAGAGTGGT GGCTTCTCCG TATCCCGGGC	720
CACAACTCCG CAGCTGACTG ATGTCTCCGA GGATTGAGC CAGCAGAGCC TGCCAAGTGA	780
ACCAGAGGAG ACCCTAAGCC GGGACCTAGG GGAGGGAGAG GAGGGAGAGC TGGCCCCCTCC	840
CGAAGACCTA CTAGGCCGTC CTCAAGCTCT GTCAAGGCAA GCCCTGGACT TGGAGGAAGA	900
GGAAGAGGAT GTGGCAGCTA AGGAAACCTT GTTGC GGCTC TCATCCCCC TCCACTTTGT	960
GAACACGCAC TTCAATGGGG CAGGGTCCCC CCCAGATGGA GTGAAATGCT CCCCTGGAGG	1020
ACCAGTGGAG AACTGAGCC CCGAGACAGT GAGTGGTGGC CTCCTGCTC TGCCCGGCAC	1080
CCTGTCACCT CCACTTTGCC TTGTTGGAAG TGACCCAGCC CCCTCCCCTT CCATTCTCCC	1140
ACCTGTTCCC CAGGACTCAC CCCAGCCCCT GCCTGCCCCCT GAGGAAGAAG AGGCACTCAC	1200
CACTGAGGAC TTTGAGTTGC TGGATCAGGG GGAGCTGGAG CAGCTGAATG CAGAGCTGGG	1260
CTTGAGCCA GAGACACCGC CAAAACCCCC TGATGCTCCA CCCCTGGGGC CCGACATCCA	1320
TTCTCTGGTA CAGTCAGACC AAGAAGCTCA GGCCGTGGCA GAGCCATGAG CCAGCCGTTG	1380

AGGAAGGAGC TGCAGGCACA GTAGGGCTTC CTGGCTAGGA GTGTTGCTGT TTCCTCCTTT 1440
 GCCTACCACT CTGGGGTGGG GCAGTGTGTG GGAAGCTGG CTGTCGGATG GTAGCTATTC 1500
 CACCYTCTGC CTGCCTGCCT GCCTGCTGTC CTGGGCATGG TGCAGTACCT GTGCCTAGGA 1560
 TTGGTTTTAA ATTTGTAAAT AATTTTCCAT TTGGGTTAGT GGATGTGAAC AGGGCTAGGG 1620
 AAGTCCTTCC CACAGCCTGC GCTTGCCTCC CTGCCTCATC TCTATTCTCA TTCCACTATG 1680
 CCCCAGCCC TGGTGGTCTG GCCCTTTCTT TTTCTCCTA TCCTCAGGGA CCTGTGCTGC 1740
 TCTGCCCTCA TGTCCCACTT GGTTGTTTAG TTGAGGCACT TTATAATTTT TCTCTTGTCT 1800
 TGTGTTCCCTT TCTGCTTTAT TTCCCTGCTG TGTCCGTGTC TTAGCAGCTC AACCCCATCC 1860
 TTTGCCAGCT CCTCCTATCC CGTGGGCACT GGCCAAGCTT TAGGGAGGCT CCTGGTCTGG 1920
 GAAGTAAAGA GTAAACCTGG GGCAGTGGGT CAGGCCAGTA GTTACACTCT TAGGTCACTG 1980
 TAGTCTGTGT AACCTTCACT GCATCCTTGC CCCATTCAGC CCGGCCTTTC ATGATGCAGG 2040
 AGAGCAGGGA TCCCGCAGTA CATGGCGCCA GCACTGGAGT TGGTGAGCAT GTGCTCTYTY 2100
 TTGAGATTAG GAGCTTCCTT ACTGCTCCTC TGGGTGATCC AAGTGATAGT GGACCCCTA 2160
 CTAGGGTCAG GAAGTGGACA CTAACATCTG TGCAGGTGTT GACTTGAAAA ATAAAGTGTT 2220
 GATTGGCTAG AAAAAAAAAA AAAAA 2245

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Ile	Ser	Tyr	Ile	Val	Leu	Leu	Ser	Ile	Leu	Leu	Trp	Pro	Leu	Val
1				5				10					15		
Val	Tyr	His	Glu	Leu	Ile	Gln	Arg	Met	Xaa	Thr	Arg	Leu	Glu	Pro	Leu
			20					25				30			
Leu	Met	Gln	Leu	Asp	Tyr	Ser	Met	Lys	Ala	Glu	Xaa	Asn	Ala	Leu	His
			35				40					45			
His	Lys	His	Asp	Lys	Arg	Lys	Arg	Gln	Gly	Lys	Asn	Ala	Pro	Pro	Gly
			50			55				60					
Gly	Asp	Glu	Pro	Leu	Ala	Glu	Thr	Glu	Ser	Glu	Ser	Glu	Ala	Glu	Leu
65					70				75					80	

Ala Gly Phe Ser Pro Val Val Asp Val Lys Lys Thr Ala Leu Ala Leu
85 90 95

Ala Ile Thr Asp Ser Glu Leu Ser Asp Glu Glu Ala Ser Ile Leu Glu
100 105 110

Ser Gly Gly Phe Ser Val Ser Arg Ala Thr Thr Pro Gln Leu Thr Asp
115 120 125

Val Ser Glu Asp Leu Asp Gln Gln Ser Leu Pro Ser Glu Pro Glu Glu
130 135 140

Thr Leu Ser Arg Asp Leu Gly Glu Gly Glu Gly Glu Leu Ala Pro
145 150 155 160

Pro Glu Asp Leu Leu Gly Arg Pro Gln Ala Leu Ser Arg Gln Ala Leu
165 170 175

Asp Leu Glu Glu Glu Glu Glu Asp Val Ala Ala Lys Glu Thr Leu Leu
180 185 190

Arg Leu Ser Ser Pro Leu His Phe Val Asn Thr His Phe Asn Gly Ala
195 200 205

Gly Ser Pro Pro Asp Gly Val Lys Cys Ser Pro Gly Gly Pro Val Glu
210 215 220

Thr Leu Ser Pro Glu Thr Val Ser Gly Gly Leu Thr Ala Leu Pro Gly
225 230 235 240

Thr Leu Ser Pro Pro Leu Cys Leu Val Gly Ser Asp Pro Ala Pro Ser
245 250 255

Pro Ser Ile Leu Pro Pro Val Pro Gln Asp Ser Pro Gln Pro Leu Pro
260 265 270

Ala Pro Glu Glu Glu Glu Ala Leu Thr Thr Glu Asp Phe Glu Leu Leu
275 280 285

Asp Gln Gly Glu Leu Glu Gln Leu Asn Ala Glu Leu Gly Leu Glu Pro
290 295 300

Glu Thr Pro Pro Lys Pro Pro Asp Ala Pro Pro Leu Gly Pro Asp Ile
305 310 315 320

His Ser Leu Val Gln Ser Asp Gln Glu Ala Gln Ala Val Ala Glu Pro
325 330 335

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTGTGGGAA GAGCTGAAGC AGGCGCTCTT GGCTCGGCGC GGCCCGCTGC AATCCGTGGA	60
GGAACGCGCC GCCGAGCCAC CATCATGCCT GGGCACTTAC AGGAAGGCTT CGGCTGCGTG	120
GTCACCAACC GATTTCGACCA GTTATTTGAC GACGAATCGG ACCCCTTCGA GGTGCTGAAG	180
GCAGCAGAGA ACAAGAAAAA AGAAGCCGGC GGGGGCGGCG TTGGGGGCCC TGGGGCCAAG	240
AGCGCAGCTC AGGCCGCGGC CCAGACCAAC TCCAACGCGG CAGGCAAACA GCTGCGCAAG	300
GAGTCCCAGA AAGACCGCAA GAACCCGCTG CCCCCAGCG TTGGCGTGTT TGACAAGAAA	360
GAGGAGACGC AGCCGCCCCG GCGCTTAAG AAAGAAGGAA TAAGACGAGT TGAAGAAGA	420
CCTGATCAAC AACTTCAGGG TGAAGGAAA ATAATTGATA GAAGACCAGA AAGGCGACCA	480
CCTCGTGAAC GAAGATTCTGA AAAGCCACTT GAAGAAAAGG GTGAAGGAGG CGAATTTTCA	540
GTTGATAGAC CGATTATTGA CCGACCTATT CGAGGTCGTG GTGGTCTTGG AAGAGGTCGA	600
GGGGGCCGTG GACGTGGAAT GGGCCGAGGA GATGGATTG ATTCTCGTGG CAAACGTGAA	660
TTTGATAGGC ATAGTGGAAG TGATAGATCT TCTTTTTCAC ATTACAGTGG CCTGAAGCAC	720
GAGGACAAAC GTGGAGGTAG CGGATCTCAC AACTGGGGAA CTGTCAAAGA CGAATTAACT	780
GACTTGATC AATCAAATGT GACTGAGGAA ACACCTGAAG GTGAAGAACA TCATCCAGTG	840
GCAGACACTG AAAATAAGGA GAATGAAGTT GAAGAGGTAA AAGAGGAGGG TCCAAAAGAG	900
ATGACTTTGG ATGAGTGGA GGCTATTCAA AATAAGGACC GGGCAAAGT AGAATTTAAT	960
ATCCGAAAAC CAAATGAAGG TGCTGATGGG CAGTGGAAGA AGGGATTTGT TCTTCATAAA	1020
TCAAAGAGTG AAGAGGCTCA TGCTGAAGAT TCGGTTATGG ACCATCATTT CCGGAAGCCA	1080
GCAAATGATA TAACGTTTCA GCTGGAGATC AATTTTGGAG ACCTTGGCCG CCCAGGACGT	1140
GGCGGCAGGG GAGGACGAGG TGGACGTGGG CGTGGTGGGC GCCCAAACCG TGGCAGCAGG	1200
ACCGACAAGT CAAGTGCTTT TGCTCCTGAT GTGGATGACC CAGAGGCATT CCCAGTTTTG	1260
GCTTAAMTGG ATGCCATAAG ACAACCCTGG TTCCTTTGTG AACCTTTTGT TTCAAAGCTT	1320
TTGCATGCTT AAGGATTCCA AACGACTAAG AAATTAAAAA AAAAAAAAAA AAAAAAAAAA	1380
AAAAAAAAAA AAAAAAAAAA AAAAAA	1406

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Pro	Gly	His	Leu	Gln	Glu	Gly	Phe	Gly	Cys	Val	Val	Thr	Asn	Arg	1	5	10	15
Phe	Asp	Gln	Leu	Phe	Asp	Asp	Glu	Ser	Asp	Pro	Phe	Glu	Val	Leu	Lys	20	25	30	
Ala	Ala	Glu	Asn	Lys	Lys	Lys	Glu	Ala	Gly	Gly	Gly	Gly	Val	Gly	Gly	35	40	45	
Pro	Gly	Ala	Lys	Ser	Ala	Ala	Gln	Ala	Ala	Ala	Gln	Thr	Asn	Ser	Asn	50	55	60	
Ala	Ala	Gly	Lys	Gln	Leu	Arg	Lys	Glu	Ser	Gln	Lys	Asp	Arg	Lys	Asn	65	70	75	80
Pro	Leu	Pro	Pro	Ser	Val	Gly	Val	Val	Asp	Lys	Lys	Glu	Glu	Thr	Gln	85	90	95	
Pro	Pro	Val	Ala	Leu	Lys	Lys	Glu	Gly	Ile	Arg	Arg	Val	Gly	Arg	Arg	100	105	110	
Pro	Asp	Gln	Gln	Leu	Gln	Gly	Glu	Gly	Lys	Ile	Ile	Asp	Arg	Arg	Pro	115	120	125	
Glu	Arg	Arg	Pro	Pro	Arg	Glu	Arg	Arg	Phe	Glu	Lys	Pro	Leu	Glu	Glu	130	135	140	
Lys	Gly	Glu	Gly	Gly	Glu	Phe	Ser	Val	Asp	Arg	Pro	Ile	Ile	Asp	Arg	145	150	155	160
Pro	Ile	Arg	Gly	Arg	Gly	Gly	Leu	Gly	Arg	Gly	Arg	Gly	Gly	Arg	Gly	165	170	175	
Arg	Gly	Met	Gly	Arg	Gly	Asp	Gly	Phe	Asp	Ser	Arg	Gly	Lys	Arg	Glu	180	185	190	
Phe	Asp	Arg	His	Ser	Gly	Ser	Asp	Arg	Ser	Ser	Phe	Ser	His	Tyr	Ser	195	200	205	
Gly	Leu	Lys	His	Glu	Asp	Lys	Arg	Gly	Gly	Ser	Gly	Ser	His	Asn	Trp	210	215	220	
Gly	Thr	Val	Lys	Asp	Glu	Leu	Thr	Asp	Leu	Asp	Gln	Ser	Asn	Val	Thr	225	230	235	240

Glu Glu Thr Pro Glu Gly Glu Glu His His Pro Val Ala Asp Thr Glu
245 250 255

Asn Lys Glu Asn Glu Val Glu Glu Val Lys Glu Glu Gly Pro Lys Glu
260 265 270

Met Thr Leu Asp Glu Trp Lys Ala Ile Gln Asn Lys Asp Arg Ala Lys
275 280 285

Val Glu Phe Asn Ile Arg Lys Pro Asn Glu Gly Ala Asp Gly Gln Trp
290 295 300

Lys Lys Gly Phe Val Leu His Lys Ser Lys Ser Glu Glu Ala His Ala
305 310 315 320

Glu Asp Ser Val Met Asp His His Phe Arg Lys Pro Ala Asn Asp Ile
325 330 335

Thr Phe Gln Leu Glu Ile Asn Phe Gly Asp Leu Gly Arg Pro Gly Arg
340 345 350

Gly Gly Arg Gly Gly Arg Gly Gly Arg Gly Arg Gly Gly Arg Pro Asn
355 360 365

Arg Gly Ser Arg Thr Asp Lys Ser Ser Ala Phe Ala Pro Asp Val Asp
370 375 380

Asp Pro Glu Ala Phe Pro Val Leu Ala
385 390

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGGACGCGG CCAGTCAGGT GCTCCTGGGC TCCGGTCTCA CCATCCTGTC CCAGCCGCTC 60

ATGTACGTGA AAGTGCTCAT CCAGGTGGGA TATGAGCCTC TTCCTCCAAC AATAGGACGA 120

AATATTTTGT GGC GGCAAGT GTGTCAGCTT CCTGGTCTCT TTAGTTATGC TCAGCACATT 180

GCCAGTATCG ATGGGAGGCG CGGGTTGTTC ACAGGCTTAA CTCCAAGACT GTGTTTCGGGA 240

GTCCTTGGA CTGTGGTCCA TGGTAAAGTT TTACAGCATT ACCAGGAGAG TGACAAGGGT 300

GAGGAGTTAG GAMCTGGAAA TGTACARAAA GAAGTCTCAT CTCCTTTGA MCACGTTATC 360

AAGGAGACAA CTCGAGAGAT GATCGCTCGT TCTGCTGCTA CCCTCATCAC ACATCCCTTC 420
CATGTTGATC ACTCTGAGAT CTATGGTACA RTTCATTGGC AGAGAATCCA AGTACTGTGG 480
ACTTTGTGAT TCCATAATAA CCATCTATCG GGAAGAGGGC ATTCTAGGAT TTTTCGCGGG 540
TCTTGTTTCT CGCCTTCTAG GTGACATCCT TTCTTTGTGG CTGTGTAACT CACTGGCCTA 600
CCTCGTCAAT ACCTATGCAC TGGACAGTGG GGTTCCTACC ATGAATGAAA TGAAGAGTTA 660
TTCTCAAGCT GTCACAGGAT TTTTGTGCGAG TATGTTGACC TATCCCTTTG TGCTTGTCTC 720
CAATCTTATG GCTGTCAACA ACTGTGGTCT TGCTGGTGGA TGCCCTCCTT ACTCCCAAT 780
ATATACGTCT TGGATAGACT GTTGGTGCAT GCTACAAAAA GAGGGGAATA TGAGCCGAGG 840
AAATAGCTTA TTTTTCGGA AGGTCCCCTT TGGGAAGACT TATTGTTGTG ACCTGAAAAT 900
GTTAATTTGA AGATGTGGGG CAGGGACAGT GACATTTCTG TAGTCCCAGA TGCACAGAAT 960
TATGGGAGAG AATGTTGATT TCTATACAGT GTGGCGCGCT TTTTAAATAA TCATTTAATC 1020
TTGGGAAAAT TCAGGTGTTT GGTGTCTGCC TTTTGTGTTT TTTTTCAG CACAACATAA 1080
CTTACCACTG ATACTCCCC TTTAGTTATT CTGAATTAGG ATATTTTGC TCCAAATTCT 1140
TATTTTACTT AACCAGAAGG GAAAAAAGT TGTATTTTCC TGAAGCTACA GGCACCTTGT 1200
CATGTGATTT TTGAGTCTCA ATTTAAGGCT TTGTAAAATG AAGAGTAGAA TTCCAAGAAA 1260
AATGAGAAAT AATTTTGTA AACTTAACAA AATCACTAAA TTAAACTATA TGGGAGGTTA 1320
TGAATTACTT TTTCTTGGGT AGACCCTAAA ATGTCAGTAG CATGCACCAG AATCTGACTC 1380
CCATTATGCT TCTAAGCACA TTTCATTGAC CTTGTCTCTC ATACTTCAAG AAAAGGACAG 1440
TACATTGCTA CATTACCCTA GAAAGTCTGT GTGAGGATCT GCCCTTCAG TCTGTTATTG 1500
CAAAGTAATA AAATGTCACC TACAGGGAGC CTCTGAGCCT ACTCTAGTTC AAGAGGCTAC 1560
CTGAAAAAAA ATAAATAAGA TAAAGGGTCA GCAACAACAA AGAAAAAGAC AATTACAGAA 1620
AATAAGCAAG ATTTGGAAAG GAAGTATAAT GGCACTTTTT TCCTCAAAGG AAGTTCTTGT 1680
TTTCACATAA AATATGAAAA GCAGATCCTG CAGGAGTAAC CCCCTTCTTT AAGAGCCAAG 1740
TATTTGCCAG TGCTTAAATT ACACCATAACC GTTCTAATTA TATATAATCT TTTGTTCTTC 1800
AGTTTTTTGT TTTGTTTCTT TTTTGTATT GTTGCCGAAG GTGAGTAGTT TTGCATTTCT 1860
GATGACAGCC TTGGAAAGTA TATTTGTAAC TCCATGTCTG GTAATGCCAA CCAAGTCGA 1920
CATGGGTCTT AGGACACTGA CCACCTCACA TGCCATACCC TCAGTTAAGC ATGTTAACAT 1980
TTATAGGAGG AAAAAATCA CTTTGGGAGA AAATAAAATT CAACTCAAGC ATAAAGCTTC 2040
TGTTTACTCA GGCCTTCTAA AAAGCAGGTT AAAATGCTCT AAAATGAGAA AGCCTGTGGT 2100

TTCAC TTATT TATATAACTC ACTGGGACAT TGCCAAATGA GTAAGCACTT AATTCGCTGC 2160
TTCTGAGACT TCTCTGTCAA AACAGCCCCA CTGATAATAT TAGACAGAAC GAGAATGCAG 2220
GGGTCTCTTC CCTCCCCTGG GGTTTAGGAA GCTCATGAGG AGCTCGGCTT AAAATGTCTT 2280
TGATGTCTCT TCCTTTGTCT CAAAAAGTAA TGTCAATTTT ATATACTATT TCAATATTAC 2340
TATCTGCATT TGTTTTAATA TAAAAATGTT TGCTGCCTAC CTTTTTCTCC CAAAAAATCT 2400
TTAAGTAAAG ATGATCTGGG AAAATGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2460
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2520
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2580
AAAAAAAAAA AAAAAAAGC GGCCGCAGGT CTAGAATTCA ATCGGAAGGT ATATAGCTTA 2640
TTTGTGCTT TTCATTGTAA TTTAACATGG TTAATGGTTA ATTACTATTT AACACACATT 2700
TCAAATGAAT ATTATTTGGG GGATTAGATT GAGTGAAATT AACCTGCTAT TAAATAGTAA 2760
ACTTTTCCTC TGGAGTCACT TTTTTCCTCC TTCAAAGTAT GTTACTGAGG AAGTAAACTT 2820
TTTTTTTTTT TTTTGGTTTT TGTTTTTTGA GACACAGTCT CGCTCTGTTG CCCAGGCTGC 2880
TGGAGTGCCG TGGCGCAATC TCGGCTCACT GCAACCTCCG CCTCCTGGAT TCAAACAATT 2940
CTCCTGCTTC AGCCTCCTGA GTAGCTGGGA TTACAGGCAC ATGCCACCAC GCCCGGCTAA 3000
TTTTTGATTT TTTAGTAGAG ACTGGGTTTC ACCATGTTGG TCAGGCTGGT CTCAAACCTC 3060
TGACCTCGTG ATCCACCCGC CTCGGCCTCC CAAATCCTG GGATTACAGG CGCGAGCCAC 3120
CACACCCGGC TGGAAGTAAA CATTTTTTAA GCTACTTTTA CTCATTCTAG CCTTG TAGAA 3180
TGACCATGTC AGCTTGAGGG ACCTAGTTCT TACCTTTTCT TGCAACCAAC ACATTGCAA 3240
TTGTGTCTGG TATGCTTGTT CCTGCTGCTA ATAAAGTAAG GCCCATTACT GTATCGGGAA 3300
TTTCTAGTGT TTCCCTGTGA ATAAACAGAT ATTTCAAGTT ACAAATCTTA AAGATTCACT 3360
AACCATCCTT TGCAGTTATT TTGGATATTT CCTTCGTGAA CAAAAATAAA ATAGGCACAT 3420
TTAGAATTCA GAGCCAATAT GTGCTTGCTT ATTAGTTTTT TAGCTAGCAA CATATTTGAA 3480
TCAGGCTGGT AATTCGGGTA ACCCAGGTAG CACAGATTTT TAATGACATA TYTAAAGATA 3540
CGTAACAGCT AAAATTTCTG CCAGTGAGAA ATTTTCCTGT TTGATATTTT TTACAAAAGA 3600
TGTTTATGTC CACCATTATY TTCATTCAGG GGCTGTGCTG AATATTTGAT AATGAGACTG 3660
ATCATTCCGC TTTTCTTTT TTAATAATAT TAGGCAGAGT TAAGCAAATT AATTATAGCT 3720
ATCTTTAAGC TATAAATGTG TTAACATGTA TATATACCAT TTATTATGTT CTACTTTAGT 3780

GATATACCTT AATTTAGTGG GCTTTGGCAG GCGGGGGGAG GGGGAACGTT CATTAATCTC 3840
 TGAGGAAAAC AAAACCTGTT TTCTACTTGA GTCTAACATA TGGTCCCAAT TTATTAATAC 3900
 TTCTGTAAAA TTTGATGTCA GGTCAACATT TTTCAGAAAT GTATTTATTC TCAGAAACAG 3960
 AACCAGAGAG AAGTTAAACA AAAGGTTATG TAACTGTTCC TTTAATGTTG TAATTGAAAA 4020
 CTTGGTTTATG CGTCTTTTTT TTCTTTCTCT TTTTTTTTCT TAAAATGCCA ACTAAAATAA 4080
 TTAGAAAGTA GCTTATTTAT TGCATGCTTA TACATTGATA TTGGAATTGG AATTGGTTGT 4140
 TAATTTCTGT TACTGGCTTT GCTAGAATTC ATATGTGCAT AAATAACACT AATATTTATC 4200
 ATCTTGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA 4237

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Tyr	Ile	Tyr	His	Leu	Leu	Cys	Ser	Thr	Leu	Val	Ile	Tyr	Leu	Asn
1				5					10					15	
Leu	Val	Gly	Phe	Gly	Arg	Ala	Gly	Glu	Gly	Glu	Arg	Ser	Leu	Ile	Ser
			20					25					30		
Glu	Glu	Asn	Lys	Thr	Cys	Phe	Leu	Leu	Glu	Ser	Asn	Ile	Trp	Ser	Gln
		35					40					45			
Phe	Ile	Asn	Thr	Ser	Val	Lys	Phe	Asp	Val	Arg	Ser	Thr	Phe	Phe	Arg
	50					55				60					
Asn	Val	Phe	Ile	Leu	Arg	Asn	Arg	Thr	Arg	Glu	Lys	Leu	Asn	Lys	Arg
65					70				75					80	
Leu	Cys	Asn	Cys	Ser	Phe	Asn	Val	Val	Ile	Glu	Asn	Leu	Val		
			85						90						

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TNTTGAAGACT GTTGCTTGTT TGGAATGT

29

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CNCCATCTAAT GGGATGATGG GTTCTTGA

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ANTTTCCGTCA CCTCGTTTCGC CTGCTGCT

29

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GNATACGAGGG GTTCCCATGG CTTCTTCT

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TNTACGACGAC ATCCAACAAT CACACTGG

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TNGTCCGGTTG GAATGAGGTG AGGCAGTG

29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "olgionucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GNTCCTCACTA TATACTTCTG GAACAACT

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GNCCTAAGAGT GTAACACTG GCCTGACC

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TNTCCTCGTGC TTCAGGCCAC TGTAATGT

29

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ANGCCCACTAA ATTAAGGTAT ATCACTAA

29

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Trp Gly Leu Gly Thr Thr Ser Ser Phe Arg Trp Tyr Ser Ser Asp

1 5 10 15
Tyr Arg Arg Ser Phe Gln Leu Asn Ser Pro Val Asp Lys Met Arg Lys
20 25 30
Thr Gly Glu Gln Ala Phe Ser Val Phe Thr Tyr Lys Val Arg Ser Val
35 40 45
Met Gly Gln
50

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO33:

AGTTGGCAGG TGGAGAGGCA GGT'TGGGAGG GAAAGTCGGG GGAGGACGCG GAAGAGGAGC 60
TGTGGGAAGG GGGAGGAGGG AGGGAGGAAA AGAGGAGGAG GCGGAGGAGA ACTGAGCAGA 120
GCAGAGCATC GAGCCAAAGG GGAGATGAGT TTGTCTGTCC TCTGCTGAGG CTACGGCCCGG 180
GCCTAGGGAA CTGGGAGCTT GGGTGGGAAGC GACACCCGTG GAAGTGGGAG GAGGTGGCGC 240
CGGGACTTTA ACCCCTTGTTG GGCTCTGCGG CAGGGGATTT AACCCTTTGT GGATCTGGCC 300
CCTCGGAGGC AGCGTCATCG GTAGTTTTAA CCCCTTCGGG GCTGGGTTTC ACGCACTGGA 360
CTTACCCTCA TCACCTTGCT CACCAACTCC TTTATTGGGG TGCTCCGCTT GGAGGTTTGA 420
GGCCACCTC CGCCATTAC GTACTGTTCC TGCCGCTGCA CCCCCTTGGA CCCGCTAGCT 480
GGCCGCACTG TGGGCGCTTA ACCCTTTACT GACTTGAGCT CCCCAGATTG CAGTTGGAGT 540
TTGCTGATAG AAGGACTAGC TAAAGGCGTC ACTGCAGGAA TTACAACTG AAGAGGACTC 600
TGTGGACTG TTTTTTTTTT CTTTTTCTTT TTTTAAAGAA AAACCCATTT TTTTCCTTAA 660
GGACTTACTA GCCAAAATTT CTTAAACTTC GAGGACTCTA CTAGCCATGG CCGAGCCATT 720
CTTGTCAGAA TATCAACACC AGCCTCAAAC TAGCAACTGT ACAGGTGCTG CTGCTGTCCA 780
GGAAGAGCTG AACCTGAGC GCCCCCAGG CGCGGAGGAG CGGGTGCCCG AGGAGGACAG 840
TAGGTGGCAA TCGAGAGCGT TCCCCAGTT GGGTGGCCGT CCGGGGCCGG AGGGGAAGG 900
GAGCCTGGAA TCCCAACCAC CTCCCTTGCA GACCCAGGCC TGTCCAGAAT CTAGCTGCCT 960

GAGAGAGGGC GAGAAGGGCC AGAATGGGA CACTCGTCC GCTGGCGGCG ACTTCCCGCC	1020
GCCGGCAGAA GTGGAACCGA CGCCCGAGGC CGAGCTGCTC GCCCAGCCTT GTCATGACTC	1080
CGAGGCCAGT AAGTTGGGGG CTCCTGCCGC AGGGGGCGAA GAGGAGTGGG GACAGCAGCA	1140
GAGACAGCTG GGAAGAAAA AACATAGGAG ACGCCCGTCC AAGAAGAAGC GGCATTGGAA	1200
ACCGTACTAC AAGCTGACCT GGGAAGAGAA GAAAAAGTTC GACGAGAAAC AGAGCCTTCG	1260
AGCTTCAAGG ATCCGAGCCG AGATGTTTCG CAAGGGCCAG CCGGTCGCGC CCTATAACAC	1320
CACGCAGTTC CTCATGGATG ATCACGACCA GGAGGAGCCG GATCTCAAAA CCGGCCGTGA	1380
CTCCAAGCGG GCCGCCGCCA AATCCGACGA CACCAGCGAT GACGACTTCA TGGAAGAAGG	1440
GGGTGAGGAG GATGGGGGCA GCGATGGGAT GGGAGGGGAC GGCAGCGAGT TTCTGCAGCG	1500
GGACTTCTCG GAGACGTACG AGCGGTACCA CACGGAGAGC CTGCAGAACA TGAGCAAGCA	1560
GGAGCTCATC AAGGAGTACC TGGAAC TGGA GAAGTGCC TC GCGCATGG AGGACGAGAA	1620
CAACCGGCTG CGGCTGGAGA GCAAGCGGCT GGGTGGCGAC GACGCGCGTG TGCGGGAGCT	1680
GGAGCTGGAG CTGGACCGGC TGCGCGCCGA GAACCTCCAG CTGCTGACCG AGAACGAACT	1740
GCACCGGCAG CAGGAGCGAG CGCCGCTTTC CAAGTTTGGA GACTAGACTG AAACTTTTTT	1800
GGGGGAGGGG GCAAAGGGGA CTTTTTACAG TGATGGAATG TAACATTATA TACATGTGTA	1860
TATAAGACAG TGGACCTTTT TATGACACAT AATCAGAAGA GAAATCCCCC TGGCTTTGGT	1920
TGGTTTCGTA AATTTAGCTA TATGTAGCTT GCGTGCTTTC TCCTGTTCTT TTAATTATGT	1980
GAAACTGAAG AGTTGCTTTT CTGTGTTTCC TTTT TAGAAG TTTT TTTTCCT TAATGTGAAA	2040
GTAATTTGAC CAAGTTATAA TGCATTTTTG TTTT TAACAA ATCCCCTCCT TAAACGGAGC	2100
TATAAGGTGG CCAAATCTGA GAACAATTAA ATTCATTTTA GTTATAATAA ATTTAATATT	2160
TGTAAATGTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2199

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Glu Pro Phe Leu Ser Glu Tyr Gln His Gln Pro Gln Thr Ser

1	5	10	15
Asn Cys Thr Gly Ala Ala Ala Val Gln Glu Glu Leu Asn Pro Glu Arg	20	25	30
Pro Pro Gly Ala Glu Glu Arg Val Pro Glu Glu Asp Ser Arg Trp Gln	35	40	45
Ser Arg Ala Phe Pro Gln Leu Gly Gly Arg Pro Gly Pro Glu Gly Glu	50	55	60
Gly Ser Leu Glu Ser Gln Pro Pro Pro Leu Gln Thr Gln Ala Cys Pro	65	70	75
Glu Ser Ser Cys Leu Arg Glu Gly Glu Lys Gly Gln Asn Gly Asp Asp	85	90	95
Ser Ser Ala Gly Gly Asp Phe Pro Pro Pro Ala Glu Val Glu Pro Thr	100	105	110
Pro Glu Ala Glu Leu Leu Ala Gln Pro Cys His Asp Ser Glu Ala Ser	115	120	125
Lys Leu Gly Ala Pro Ala Ala Gly Gly Glu Glu Glu Trp Gly Gln Gln	130	135	140
Gln Arg Gln Leu Gly Lys Lys Lys His Arg Arg Arg Pro Ser Lys Lys	145	150	155
Lys Arg His Trp Lys Pro Tyr Tyr Lys Leu Thr Trp Glu Glu Lys Lys	165	170	175
Lys Phe Asp Glu Lys Gln Ser Leu Arg Ala Ser Arg Ile Arg Ala Glu	180	185	190
Met Phe Ala Lys Gly Gln Pro Val Ala Pro Tyr Asn Thr Thr Gln Phe	195	200	205
Leu Met Asp Asp His Asp Gln Glu Glu Pro Asp Leu Lys Thr Gly Leu	210	215	220
Tyr Ser Lys Arg Ala Ala Ala Lys Ser Asp Asp Thr Ser Asp Asp Asp	225	230	235
Phe Met Glu Glu Gly Gly Glu Glu Asp Gly Gly Ser Asp Gly Met Gly	245	250	255
Gly Asp Gly Ser Glu Phe Leu Gln Arg Asp Phe Ser Glu Thr Tyr Glu	260	265	270
Arg Tyr His Thr Glu Ser Leu Gln Asn Met Ser Lys Gln Glu Leu Ile	275	280	285
Lys Glu Tyr Leu Glu Leu Glu Lys Cys Leu Ser Arg Met Glu Asp Glu	290	295	300
Asn Asn Arg Leu Arg Leu Glu Ser Lys Arg Leu Gly Gly Asp Asp Ala	305	310	315
			320

Arg Val Arg Glu Leu Glu Leu Glu Leu Asp Arg Leu Arg Ala Glu Asn
325 330 335

Leu Gln Leu Leu Thr Glu Asn Glu Leu His Arg Gln Gln Glu Arg Ala
340 345 350

Pro Leu Ser Lys Phe Gly Asp
355

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGCTAGGCCG CGAGCTTAGT CCTGGGAGCC GCCTCCGTCG CCGCCGTCAG AGCCGCCCTA 60
TCAGATTATC TTAACAAGAA AACCAACTGG AAAAAAAAAAAT GAAATTCCTT ATCTTCGCAT 120
TTTTCGGTGG TGTTACCTT TTATCCCTGT GCTCTGGGAA AGCTATATGC AAGAATGGCA 180
TCTCTAAGAG GACTTTTGAA GAAATAAAAG AAGAAATAGC CAGCTGTGGA GATGTTGCTA 240
AAGCAATCAT CAACCTAGCT GTTTATGGTA AAGCCCAGAA CAGATCCTAT GAGCGATTGG 300
CACTTCTGGT TGATACTGTT GGACCCAGAC TGAGTGGCTC CAAGAACCTA GAAAAAGCCA 360
TCCAAATTAT GTACCAAAAC CTGCAGCAAG ATGGGCTGGA GAAAGTTCAC CTGGAGCCAG 420
TGAGAATACC CCACTGGGAG AGGGGAGAAG AATCAGCTGT GATGCTGGAG CCAAGAATTC 480
ATAAGATAGC CATCCTGGGT CTTGGCAGCA GCATTGGGAC TCCTCCAGAA GGCATTACAG 540
CAGAAGTTCT GGTGGTGACC TCTTTCGATG AACTGCAGAG AAGGGCCTCA GAAGCAAGAG 600
GGAAGATTGT TGTTTATAAC CAACCTTACA TCAACTACTC AAGGACGGTG CAATACCGAA 660
CGCAGGGGGC GGTGGAAGCT GCCAAGGTGG GGGCTTTGGC ATCTCTCATT CGATCCGTGG 720
CCTCCTTCTC CATCTACAGT CCTCACACAG GTATTCAGGA ATACCAGGAT GGCGTGCCCA 780
AAATTCCAAC AGCCTGTATT ACGGTGGAAG ATGCAGAAAT GATGTCAAGA ATGGCTTCTC 840
ATGGGATCAA AATTGTCATT CAGCTAAAGA TGGGGGCAAA GACCTACCCA GATACTGATT 900
CCTTCAACAC TGTAGCAGAG ATCACTGGGA GCAAATATCC AGAACAGGTT GTACTGGTCA 960
GTGGACATCT GGACAGCTGG GATGTTGGGC AGGGTGCCAT GGATGATGGC GGTGGAGCCT 1020
TTATATCATG GGAAGCACTC TCACCTATTA AAGATCTTGG GCTGCGTCCA AAGAGGACTC 1080

TGCGGCTGGT GCTCTGGACT GCAGAAGAAC AAGGTGGAGT TGGTGCCTTC CAGTATTATC 1140
 AGTTACACAA GGTAATATT TCCAACCTACA GTCTGGTGAT GGAGTCTGAC GCAGGAACCT 1200
 TCTTACCCAC TGGGCTGCAA TTTACTGGCA GTGAAAAGGC CAGGGCCATC ATGGAGGAGG 1260
 TTATGAGCCT GCTGCAGCCC CTCAATATCA CTCAGGTCCT GAGCCATGGA GAAGGGACAG 1320
 ACATCAACTT TTGGATCCAA GCTGGAGTGC CTGGAGCCAG TCTACTTGAT GACTTATACA 1380
 AGTATTTCTT CTTCCATCAC TCCCACGGAG ACACCATGAC TGTCATGGAT CCAAAGCAGA 1440
 TGAATGTTGC TGCTGCTGTT TGGGCTGTTG TTTCTTATGT TGTTCAGAC ATGGAAGAAA 1500
 TGCTGCCTAG GTCCTAGAAA CAGTAAGAAA GAAACGTTTT CATGCTTCTG GCCAGGAATC 1560
 CTGGGTCTGC AACTTTGGAA AACTCCTCTT CACATAACAA TTTCATCCAA TTCATCTTCA 1620
 AAGCACAACCT CTATTTTCATG CTTTCTGTGA TTATCTTTCT TGATACTTTC CAAATTCTCT 1680
 GATTCTAGAA AAAGGAATCA TTCTCCCCTC CCTCCCACCA CATAGAATCA ACATATGGTA 1740
 GGGATTACAG TGGGGGCATT TCTTTATATC ACCTCTTAAA AACATTGTTT CCACTTTAAA 1800
 AGTAAACACT TAATAAATTT TTGGAAGATC TCTGAAAAAA AAAAAAAAAA A 1851

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
 1 5 10 15
 Leu Cys Ser Gly Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr
 20 25 30
 Phe Glu Glu Ile Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys
 35 40 45
 Ala Ile Ile Asn Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr
 50 55 60
 Glu Arg Leu Ala Leu Leu Val Asp Thr Val Gly Pro Arg Leu Ser Gly
 65 70 75 80
 Ser Lys Asn Leu Glu Lys Ala Ile Gln Ile Met Tyr Gln Asn Leu Gln
 85 90 95

Gln Asp Gly Leu Glu Lys Val His Leu Glu Pro Val Arg Ile Pro His
100 105 110
Trp Glu Arg Gly Glu Glu Ser Ala Val Met Leu Glu Pro Arg Ile His
115 120 125
Lys Ile Ala Ile Leu Gly Leu Gly Ser Ser Ile Gly Thr Pro Pro Glu
130 135 140
Gly Ile Thr Ala Glu Val Leu Val Val Thr Ser Phe Asp Glu Leu Gln
145 150 155 160
Arg Arg Ala Ser Glu Ala Arg Gly Lys Ile Val Val Tyr Asn Gln Pro
165 170 175
Tyr Ile Asn Tyr Ser Arg Thr Val Gln Tyr Arg Thr Gln Gly Ala Val
180 185 190
Glu Ala Ala Lys Val Gly Ala Leu Ala Ser Leu Ile Arg Ser Val Ala
195 200 205
Ser Phe Ser Ile Tyr Ser Pro His Thr Gly Ile Gln Glu Tyr Gln Asp
210 215 220
Gly Val Pro Lys Ile Pro Thr Ala Cys Ile Thr Val Glu Asp Ala Glu
225 230 235 240
Met Met Ser Arg Met Ala Ser His Gly Ile Lys Ile Val Ile Gln Leu
245 250 255
Lys Met Gly Ala Lys Thr Tyr Pro Asp Thr Asp Ser Phe Asn Thr Val
260 265 270
Ala Glu Ile Thr Gly Ser Lys Tyr Pro Glu Gln Val Val Leu Val Ser
275 280 285
Gly His Leu Asp Ser Trp Asp Val Gly Gln Gly Ala Met Asp Asp Gly
290 295 300
Gly Gly Ala Phe Ile Ser Trp Glu Ala Leu Ser Leu Ile Lys Asp Leu
305 310 315 320
Gly Leu Arg Pro Lys Arg Thr Leu Arg Leu Val Leu Trp Thr Ala Glu
325 330 335
Glu Gln Gly Gly Val Gly Ala Phe Gln Tyr Tyr Gln Leu His Lys Val
340 345 350
Asn Ile Ser Asn Tyr Ser Leu Val Met Glu Ser Asp Ala Gly Thr Phe
355 360 365
Leu Pro Thr Gly Leu Gln Phe Thr Gly Ser Glu Lys Ala Arg Ala Ile
370 375 380
Met Glu Glu Val Met Ser Leu Leu Gln Pro Leu Asn Ile Thr Gln Val
385 390 395 400
Leu Ser His Gly Glu Gly Thr Asp Ile Asn Phe Trp Ile Gln Ala Gly

	405	410	415
Val Pro Gly Ala Ser Leu Leu Asp Asp Leu Tyr Lys Tyr Phe Phe Phe			
420	425	430	
His His Ser His Gly Asp Thr Met Thr Val Met Asp Pro Lys Gln Met			
435	440	445	
Asn Val Ala Ala Ala Val Trp Ala Val Val Ser Tyr Val Val Ala Asp			
450	455	460	
Met Glu Glu Met Leu Pro Arg Ser			
465	470		

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGAAGTTCA AGGGCCCCCG GCCTCCTGCG CTCCTGCCGC CGGGACCCTC GACCTCCTCA	60
GAGCAGCCGG CTGCCGCCCC GGGAAGATGG CGAGGAGGAG CCGCCACCGC CTCCTCCTGC	120
TGCTGCTGCG CTACCTGGTG GTCGCCCTGG GCTATCATAA GGCCTATGGG TTTTCTGCCC	180
CAAAAGACCA ACAAGTAGTC ACAGCAGTAG AGTACCAAGA GGCTATTTTA GCCTGCAAAA	240
CCCCAAAGAA GACTGTTTCC TCCAGATTAG AGTGGAAGAA ACTGGGTCGG AGTGTCTCCT	300
TTGTCTACTA TCAACAGACT CTTCAGGTG ATTTTAAAAA TCGAGCTGAG ATGATAGATT	360
TCAATATCCG GATCAAAAAT GTGACAAGAA GTGATGCGGG GAAATATCGT TGTGAAGTTA	420
GTGCCCCATC TGAGCAAGGC CAAAACCTGG AAGAGGATAC AGTCACTCTG GAAGTATTAG	480
TGGCTCCAGC AGTTCCATCA TGTGAAGTAC CCTCTTCTGC TCTGAGTGGA ACTGTGGTAG	540
AGCTACGATG TCAAGACAAA GAAGGGAATC CAGCTCCTGA ATACACATGG TTTAAGGATG	600
GCATCCGTTT GCTAGAAAAT CCCAGACTTG GCTCCCAAAG CACCAACAGC TCATACACAA	660
TGAATACAAA AACTGGAACT CTGCAATTTA ATACTGTTTC CAACTGGAC ACTGGAGAAT	720
ATTCTGTGA AGCCCGCAAT TCTGTTGGAT ATCGCAGGTG TCCTGGGAAA CGAATGCAAG	780
TAGATGATCT CAACATAAGT GGCATCATAG CAGCCGTAGT AGTTGTGGCC TTAGTGATTT	840
CCGTTTGTGG CCTTGGTGTA TGCTATGCTC AGAGGAAAGG CTACTTTTCA AAAGAAACCT	900

CCTTCCAGAA GAGTAATTCT TCATCTAAAG CCACGACAAT GAGTGAAAAT GATTTCAAGC 960
 ACACAAAATC CTTTATAATT TAAAGACTCC ACTTTAGAGA TACACCAAAG CCACCGTTGT 1020
 TACACAAGTT ATTAAACTAT TATAAACTC AAAAAAAAAA AAAAAAAAAA AAAAAA 1076

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 298 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr
 1 5 10 15
 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30
 Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp

195	200	205
Thr Gly Glu Tyr Ser Cys Glu	Ala Arg Asn Ser Val Gly Tyr Arg Arg	
210	215	220
Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile		
225	230	235
Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu		
245	250	255
Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser		
260	265	270
Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn		
275	280	285
Asp Phe Lys His Thr Lys Ser Phe Ile Ile		
290	295	

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAAAGGTTGT GTAGCTTGCC CTGGTTGCAT AGTTAAACGA GGGCTAGAAA CAGGACTAGG	60
AGTCAGGCCT GTCCAGCTGG AAAACTTGGG TTTTCTAGAA GGGGTACCCT GGCCTCCTGC	120
GGAGCCTGCT GTGGGACTCT GCAGAACACA ATTCAAGGCC AGACTGAACA CTAGCCTGAA	180
CCTGCCCTGA GAATCCCTCT AAGCCGACCT ACTCCACAGC TGTCTGACT GTGTAAGCGA	240
GATGATGATT AGTGATCAGA CGAAAGGATT CCTGTGATTG GTAACCCTCT CAAAGTATTT	300
GGAAAACAGT TCAATTTTCA TCTATTTTCAG AAGCACGCCG TGGTGTCTAT TGAGGCTCAC	360
CTGCATTGAA TTCCTTCCTT TTTATGTTGC GATCTCCCAA GATTGCATTG TGGAGTGTTT	420
TCGAATCCAT TTTGAAATCC CCGTGCGTGC GCTATGCAGG CCTCAGTCTT TTTCCATTCC	480
ATTCTTAACT CTACTTTTCA CGGAAGCAGT GTTTTACCCC GACACTGGCT TGCCTAGGAC	540
CTTGTGCTCT GCACAACTAG CAGGGCCCGG CAGGATGTAC TGAATTCTTG CTCTCGTGTC	600
CAGCTGGACG GTGATGGCTT TCAAGTCCTT GGCTGTTGGG AGCTTACTAT AAATGTTCGT	660
CTTGGCTACA AACTCTCCAC TCTTTCCTCG GCACTCTCTC AGCATTGCCA CCACTGTCTT	720

TCCTCTTGGC CAACTGTTTT CTTTACTTAG GCTTTCCTT GCTAGAAAGT CCAGGTAAC 780

TTCTCCACGG GACCTGGTTT CCTTCGCACA TCCCAGCTGG CCTCGAGGAA AGGTAGCTCT 840

TCCAAATCAG AGAATCTGGA TGCTGGGCTG GGCTCTGCAC CAACCAGCTG GGCCGCTTCA 900

CCCGCTGGGC CCCAAACTAC TCATCTGTGA AGCGAAGGCA CCGCGCTTGA TGCCTTCTGC 960

AACGTTCTTC AGTTTGAAAA TCCTTCTGTT TCGTTGGGGA TATTTACGG CCTCTTCTCA 1020

AGGTTGCACT TTTGCCAGCT GCCAGGGATC GTCTCAAAAC AGGTTCTTAG TGCATTCATA 1080

GCTTGAGCTG CTGTCTTGAA AGTAGTACAT TCCTTTTTCT GCCAACTTTT TTCTGAGAAA 1140

GTTTTTGAAT GCACACGTGC ACCCAACAGA GTGAGAGTGG CTGTTAAGAG AGAGGGCGCC 1200

ATTTCTTTTG CCCTCCAGCC TGTCCCTGTG CACCCTGGAG GGGCCCGTTT TTTCCACCGC 1260

TTAGATAAAA TCTAGGGCAA GTTCCTGAAC TTCTCTTGTC TCTCTCAGGT AACAAAAATT 1320

CTTTTGGGCT CCTTTAGTCA CAAAGATATT CACGATTTCA GGTATTAAAG TGCCAGCCC 1380

TGGGTGATTG TCAAAATTCT GAACCTGATT TAAAGTGGCA CCTCCTCTCA CAGTCTTCGG 1440

GAGGGAGAGA CCGGAGCCAG GAGTGCAGCG TGTGTGCTGG GGTCTGTCGT GGCCCACTCC 1500

ACACCTGCTG GGTGGATCCG GCTGGTGCCC CATGGGCGCC TCTGAGATGC CCCTCCCCAC 1560

CCCATCAGTG GCGCTGTCTC ACCTGCAGGC TGTCTCACA GGTGGTCCCC CCTCACTCCT 1620

CCTGCAGCCC CAGTTCCTGG CTGTTTATTG TTATTGGGAC CCGTCACCCT CCTGGAGGCG 1680

GTCCCAGCCG AGCCCCCTTA AGACAGCACC AGGCTGGCTC CACTTGCCCC CCGCTGGTTC 1740

AGGGAAGTGC TGCTGCAGCC GTTTAGTTTG ACAAAGGAGG CAGCGAGGCC GTCTCATTGG 1800

TAGCCCTCTC CTGGCTTGCC CAGCCACCAC CTCACCTCGA TTCCTCCCAG GCCTGGGTCC 1860

AGCACCAGCC TAGGAAGAGG GTGCCCCATG CTGTCTAGCT CTTCTTCGGG ATGGGGGGCT 1920

CCAGGTTTCT TGGTATTTTG CTTTGGCCTT TGGAGCCTCA GTCAAACTG AGGAAAGGTG 1980

TCATTTTCAC ATCTCGTCAC ACGTACAGTG ACTGCAACTA AAAGCACAGG CTTTGTAGAA 2040

ACAGACATGG GTTCAGGCCC CAGCTCCACC ATTCAACAAG TGTGTGGCTT CCTGCAAGGT 2100

ACCTTCATCT CTGAGTTACC TGACTCCATC TGAGTTTCCT TCTTGTAATA CTGGCATCCA 2160

TGAAAGTGGC TACCTCGAAG GGCGTGAAGA TGAAATGAGG TGGAAAGTAG GTAGCCCCCG 2220

AATGAGGGAA GCATTGAGTG AGAGCTGGCC CTCTGACCCT TCTAAAAGAA CACAGCCAAC 2280

TTTTTAACT GTCTTTCCAG AAAGAGATGG AAAACTTCGA AGCCCTTTT CACTGCCTTG 2340

CCAAGCAGTT CCACCAGCTG TACCGGGAGA AGGTGGAGGT TTTCCGGGCC CTGGCATGAC 2400

GAGCTGGAGC AGATCGTGCT GCACAACCGG AGAAGACAGA ATTACCTCTG CTCTTTTAAT 2460

ATATAATGAT GGCTTTAAAT AAAATTAGGA GAAAATGTCA AAAAAAAAAA AAAAAAAAAA 2520
AA 2522

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Met Ile Ser Asp Gln Thr Lys Gly Phe Leu Ser Leu Val Thr Leu
1 5 10 15
Ser Lys Tyr Leu Glu Asn Ser Ser Ile Phe Ile Tyr Phe Arg Ser Thr
20 25 30
Pro Trp Cys Leu Leu Arg Leu Thr Cys Ile Glu Phe Leu Pro Phe Tyr
35 40 45
Val Ala Ile Ser Gln Asp Cys Ile Val Glu Cys Phe Arg Ile His Phe
50 55 60
Glu Ile Pro Val Arg Ala Leu Cys Arg Pro Gln Ser Phe Ser Ile Pro
65 70 75 80
Phe Leu Thr Leu Leu Ser Thr Glu Ala Val Phe Tyr Pro Asp Thr Gly
85 90 95
Leu Pro Arg Thr Leu Cys Ser Ala Gln Leu Ala Gly Pro Gly Arg Met
100 105 110
Tyr

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1962 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCGGGCCCC AGCCTTCTCC AGAACCCCTG CTACCCACGA CTAAGCCCCG AACAATCTGC 60
CCTTGGGCTT GTTCTCTTCG CAGTTGTCGG CCCTGGGCGG GGAGCTGGAG TCCCAGACTC 120

ATAGGTCCCG	CCCCAGCCCC	CGAAGAGCCG	CCTCAGCCGG	GGGGAGTTGC	TCGGACTCAA	180
ACGTCCAGTC	CTCGTGCGAC	CGCGCTGGGT	CGGAAGTGAG	CAGGCTGAGG	CCACCATGGA	240
GCAGTGTGCG	TGCGTGGAGA	GAGAGCTGGA	CAAGGTCCTG	CAGAAGTTCC	TGACCTACGG	300
GCAGCACTGT	GAGCGGAGCC	TGGAGGAGCT	GCTGCACTAC	GTGGGCCAGC	TGCGGGCTGA	360
GCTGGCCAGC	GCAGCCCTCC	ARGGGACCCC	TCTCTCAGCC	ACCTCTCTCT	TGGTGATGTC	420
ACAGTGCTGC	CGGAAGATCA	AAGATACGGT	GCAGAACTG	GCTTCGGAMC	ATAAGGACAT	480
TCACAGCAGT	GTATCCCGAG	TGGGCAAAGC	CATTGACAGG	AACTTCGACT	CTGAGATCTG	540
TGGTGTTGTG	TCAGATGCGG	TGTGGGACGC	GCGGGAACAG	CAGCAGCAGA	TCCTGCAGAT	600
GGCCATCGTG	GAACACCTGT	ATCAGCAGGG	CATGCTCAGC	GTGGCCGAGG	AGCTGTGCCA	660
GGAATCAACG	CTGAATGTGG	ACTTGATTTT	CAAGCAGCCT	TTCCTAGAGT	TGAATCGAAT	720
CCTGGAAGCC	CTGCACGAAC	AAGACCTGGG	TCCTGCGTTG	GAATGGGCCG	TCTCCACAG	780
GCAGCGCCTG	CTGGAActCA	ACAGCTCCCT	GGAGTTCAAG	CTGCACCGAC	TGCACTTCAT	840
CCGCCTCTTG	GCAGGAGGCC	CCGCGAAGCA	GCTGGAGGCC	CTCAGCTATG	CTCGGCACTT	900
CCAGCCCTTT	GCTCGGCTGC	ACCAGCGGGA	GATCCAGGTG	ATGATGGGCA	GCCTGGTGTA	960
CCTGCGGCTG	GGCTTGAGAG	AGTCACCCTA	CTGCCACCTG	CTGGACAGCA	GCCACTGGGC	1020
AGAGATCTGT	GAGACCTTTA	CCCGGGACGC	CTGTTCCCTG	CTGGGGCTTT	CTGTGGAGTC	1080
CCCCCTTAGC	GTCAGCTTTG	CCTYTGGCTG	TGTGGCGCTG	CCTGTGTTGA	TGAACATCAA	1140
GGCTGTGATT	GAGCAGCGGC	AGTGCACTGG	GGTCTGGAAT	CACAAGGACG	AGTTACCGAT	1200
GAGATTGAAC	TAGGCATGAA	GTGCTGGTAC	CACTCCGTGT	TCGCTTGCCC	CATCCTCCGC	1260
CAGCAGACGT	CAGATTCCAA	CCCTCCCATC	AAGCTCATCT	GTGGCCATGT	TATCTCCCGA	1320
GATGCACTCA	ATAAGCTCAT	TAATGGAGGA	AAGCTGAAGT	GTCCCTACTG	TCCCATGGAG	1380
CAGAACCCCG	CAGATGGGAA	ACGCATCATA	TTCTGATTCC	TACCTGGAAG	GAATTTTGTT	1440
GAAAGGGGTT	TTCACCTGTG	AGCCTTGGTC	TGTCTCGGTA	GGGTGGTCAA	CTTCAGTGGA	1500
CTGTGGTTGG	TTTCAGAGCG	CCTGGCTGAG	GAGTTCCACT	GAGGGGAGCA	CTGGAGCAGC	1560
CCTTTGGCAG	AGGCTGAGGA	GGGAGATGGA	CCAGCCCACG	CCTGGCACCT	GGCTCCATGG	1620
CATAAGGAAA	GGGAGATGCT	GGCCTCTGTG	CTCCTGCTGT	CTTTTCCTGT	TTCTGTTTGC	1680
GTTTGACTTA	GTAGCAACCG	ACAGAGTGGC	AAGGGATTGT	GTCTTCAGCA	GTAGACATCC	1740
TTCCACCCCT	GCCCTCAGCC	AAGTCTCTTG	CTGCCATGCC	AATGCTATGT	CCACCCTTGC	1800

CCCTCGGCCC AAGAGTGTCC AGCGGTGGCC CACYTYTTCC TCCCACTACA GCCTCAACAG 1860
TATGTACCAT CTCCCACTGT AAATAGTCCC AGTTAGAACG GAATGCCGTT GTTTTATAAC 1920
TTTGAACAAA TGTATTTACT GCCAAAAAAA AAAAAAAAAA AA 1962

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Glu Gln Cys Ala Cys Val Glu Arg Glu Leu Asp Lys Val Leu Gln
1 5 10 15
Lys Phe Leu Thr Tyr Gly Gln His Cys Glu Arg Ser Leu Glu Glu Leu
20 25 30
Leu His Tyr Val Gly Gln Leu Arg Ala Glu Leu Ala Ser Ala Ala Leu
35 40 45
Gln Gly Thr Pro Leu Ser Ala Thr Leu Ser Leu Val Met Ser Gln Cys
50 55 60
Cys Arg Lys Ile Lys Asp Thr Val Gln Lys Leu Ala Ser Xaa His Lys
65 70 75 80
Asp Ile His Ser Ser Val Ser Arg Val Gly Lys Ala Ile Asp Arg Asn
85 90 95
Phe Asp Ser Glu Ile Cys Gly Val Val Ser Asp Ala Val Trp Asp Ala
100 105 110
Arg Glu Gln Gln Gln Gln Ile Leu Gln Met Ala Ile Val Glu His Leu
115 120 125
Tyr Gln Gln Gly Met Leu Ser Val Ala Glu Glu Leu Cys Gln Glu Ser
130 135 140
Thr Leu Asn Val Asp Leu Asp Phe Lys Gln Pro Phe Leu Glu Leu Asn
145 150 155 160
Arg Ile Leu Glu Ala Leu His Glu Gln Asp Leu Gly Pro Ala Leu Glu
165 170 175
Trp Ala Val Ser His Arg Gln Arg Leu Leu Glu Leu Asn Ser Ser Leu
180 185 190
Glu Phe Lys Leu His Arg Leu His Phe Ile Arg Leu Leu Ala Gly Gly
195 200 205

Pro Ala Lys Gln Leu Glu Ala Leu Ser Tyr Ala Arg His Phe Gln Pro
 210 215 220

Phe Ala Arg Leu His Gln Arg Glu Ile Gln Val Met Met Gly Ser Leu
 225 230 235 240

Val Tyr Leu Arg Leu Gly Leu Glu Lys Ser Pro Tyr Cys His Leu Leu
 245 250 255

Asp Ser Ser His Trp Ala Glu Ile Cys Glu Thr Phe Thr Arg Asp Ala
 260 265 270

Cys Ser Leu Leu Gly Leu Ser Val Glu Ser Pro Leu Ser Val Ser Phe
 275 280 285

Ala Xaa Gly Cys Val Ala Leu Pro Val Leu Met Asn Ile Lys Ala Val
 290 295 300

Ile Glu Gln Arg Gln Cys Thr Gly Val Trp Asn His Lys Asp Glu Leu
 305 310 315 320

Pro Met Arg Leu Asn
 325

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AAAAACACAA AACCCCGTAA AATCACAAAG AAAATCCAAC ACCAAAGGCG CAGAAGCCGG	60
CTGGCCGTGG TGGGGGCAGC GTAGGCGTAG CATCCCTCTC CTCTCACTTA GCCTGTTGAC	120
TCTTGTTATT ATCATGATAT TCACAAAACG CCGCATGTTT AAAAAGTCAT AGATGTCATC	180
TTCTCTCTGC CCCAGGGAG GAAAGCCACC TTCTCTTGCC CCTTGGCCCC TTTGTCAGGG	240
GCCAGGGGTC TGCCGGGTGG GGGTGCCAAC AGGCCTGGCC CTTTCTCTCC CTGCATCCAG	300
CCATGGGGGC CTCTGCGATT GCCGGAAGGT TGCATGGCTG GTCCCAGGGC CAGCACAGGC	360
CCGAGGCCGG GCTGCCTGGT TTTATTTTTA TTAACTTTA TTTTCTGTTT TATGAGTGTG	420
TGTCCGCCCA CCCCCACCCC CTTCAGTGTT AAGTGGGGAG CCCTGGGGGA GTCTCTCCTG	480
CCTCCCAGCC TCTCCAAGA CCTCCCCCCT CGTCACCAGC CATCCCTCTG GACCAGGCAG	540

AGGGCGGACC GGGTGGGCAG GGGCCTGAGG GTGGCTCGGG CCAGCCCACC AGCCAATGGA 600
 CCCCTCCTCA GGCCGCCAGT GTCGCCCTGC CCCTTTTAA AACAAAATGC CCTCGTTTGT 660
 AAACCCTTAG ACGCTTGAGA ATAAACCCCT TCCTTTTCTT CCAAAAAAAAA AAAAAAAAAA 720
 AAAAAAAAAA AAAAAAAAAA AAAAA 745

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Ala Gly Pro Arg Ala Ser Thr Gly Pro Arg Pro Gly Cys Leu Val
 1 5 10 15
 Leu Phe Leu Phe Asn Phe Ile Phe Cys Phe Met Ser Val Cys Pro Pro
 20 25 30
 Thr Pro Thr Pro Phe Ser Val Lys Trp Gly Ala Leu Gly Glu Ser Leu
 35 40 45
 Leu Pro Pro Ser Leu Ser Gln Asp Leu Pro Pro Arg His Gln Pro Ser
 50 55 60
 Leu Trp Thr Arg Gln Arg Ala Asp Arg Val Gly Arg Gly Leu Arg Val
 65 70 75 80
 Ala Arg Ala Ser Pro Pro Ala Asn Gly Pro Leu Leu Arg Pro Pro Val
 85 90 95
 Ser Pro Cys Pro Phe Leu Lys Gln Asn Ala Leu Val Cys Lys Pro Leu
 100 105 110
 Asp Ala

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1983 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGGCAATAGT	GGTTAGGGAA	GGCTCCTTTG	AGGAAGTGAA	TTTTTAGCTG	AGACTTAAAG	60
AACAAATGAG	ATTTAGCTAG	AAAAATTGGA	CATGCGATGC	CAAGATGGCA	TTTTAAAAGA	120
ATAATAGTAA	GCACAAAGGC	CCTGTAGCAG	GAGGGAGCTG	ATTGTCCATA	GTTCAGACAG	180
CAAAGAAGCT	GATGATGCAG	GTTGGGGTCA	GACCGTGTTT	GACTACAGAT	AGGATGTAA	240
GGGTTTTGGC	TTTTTAGGTT	TTTGTTTTAA	TTCTAAAAGT	AATGGAAAAT	GTACTCCTTT	300
TGGTGGTGGT	CTGAGAGAAAG	GTACATCATT	AGAATGACAT	TTTGAAAACA	ACACTCAGGC	360
TGCTCAGTAG	AGAATGGCTT	CAAAGGATTT	AAAAGCAGAA	GCAGAAGGAC	ATATTAGAGA	420
AGGATTGTAT	AGTTTTCTGG	TAAAAGATGA	CAGTGAATTG	TATGGGCGAT	GGATTAGCCG	480
TGGAAGGTGT	TGAGTATAAG	TGGTCTCCAG	CCAAACTCTA	TGGTTACTGG	AATAAGAGAG	540
TAGGAACCCCT	TCTCAGGCTT	TATCTTTATC	TATTCTTGTC	AACAGTATGT	ACATGTGTCC	600
CCCAGCCCCA	AATAACTGTA	CAGTTTAATG	ATGTTCACTC	TATACAGTTC	CCAGAATCCA	660
TTGGAAATTG	CTGTAACAGC	ATATCCTCAA	TGCCCATCAA	TTCTCCACGT	CCAACCTCTC	720
CATGGCCTCC	TCTGCCTCTG	CTGATCTGTG	AACTTCCCAA	GCCCCTTCCC	CTACCTGCTT	780
TTGATTGGCT	TTAACTTTTA	CAATATCTTC	ATTACTCCAA	GTTTGTTCAA	CATCCTTTTT	840
ATTTTTTTAA	ATCATAGATT	GATTTAGTTT	ATTCTCTTTG	CCATTTTTGA	ATCTCATTAT	900
TTCTGTTTCT	CCTTGTTTAT	TAGTGGCTCT	GTTTTCCCTC	AATTGCCTCT	TGCTTTTGAG	960
AAGCTCTTGT	GATTCTTTTA	GGGCCATTTG	CCATTGATT	GGTTTGTCTT	CCTTTTCCCT	1020
ATAAGCTTTA	AATATGGCAT	TATAGTTTTA	TCCCCTTTCC	TCTTCTTTAG	GTACAACCTGC	1080
AGACACTTTG	CTCTTCCAAG	GTTACTAAGC	AGTGTCTGAC	ACAATGTAGA	AGCTCAACAA	1140
ATATTGGTTA	AATTTATTTT	TTCTATTGAT	TGTTCAAGCT	TTGATGACAT	CACCTAAAAT	1200
GTTTCTTGTA	CACACCCTGT	TTTCTACTGA	TATATGTATG	TGTATGGCTA	CCTGAATCCA	1260
GGTTTCTTCT	AGGAATATAC	AGAAAGTAAT	TGATTTCTCT	GTGGATCTCT	AACAGTGACA	1320
AGAATTTTCA	CCTATGCCTG	TGAGAATACC	TTCAAAAGTA	TTGGGTGCTC	ATCATAAACA	1380
CACATCAGTT	TAACAAACTC	TTATGGATGC	ATTGACTTTC	CCAGTTAGTT	GCTAGATGAC	1440
TTCGGATGAT	TTGCATAATG	GGTCTCAGTT	TCCATATCTG	TTAAATGGCA	ATAATCAGAG	1500
AATTTTAAAA	AATTTAAGGA	CACCTGGAAA	GCTTGAAAGA	TCCCTAGAAA	GCATGTGTTT	1560
ATTCCACATA	GTGGGAACTA	TGCTAGATTTC	CCAAAGACAC	AAAGACAACT	AAGACAACTT	1620

AGAATAAGAA GGAAAAGAGA ATGATTCGTT GCAATGATCC CCTTGAAGCT CCAGTTGAAA 1680
 GTCAGAGTAT TGCCCTGGAT TGGAAGTAGT CTCCAAACTG ACATCATTTT CTTTTTCGAA 1740
 CCATATCTGG CCTGTCTCTC TTGCCAGTTG CATATTAAAG GTAACAGATT TGAAAATGTT 1800
 TGGAATAAAA GCTCTAGTTA GGTGTGGTGG CACACACCTG CCATCCCAGC TACTGGAGAG 1860
 TCTGAGACTC GATGATTGTT TCAGCCCAAG AGTTGGAGGT TGTAGTGAGC TATGATGGCA 1920
 CCACTGCACT CCAGTCTGTG TGACAGAGCG AAGACCTTGT CTCTAAGGAA AAAAAAAAAA 1980
 AAA 1983

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Thr Val Asn Cys Met Gly Asp Gly Leu Ala Val Glu Gly Val Glu
 1 5 10 15
 Tyr Lys Trp Ser Pro Ala Lys Leu Tyr Gly Tyr Trp Asn Lys Arg Val
 20 25 30
 Gly Thr Leu Leu Arg Leu Tyr Leu Tyr Leu Phe Leu Ser Thr Val Cys
 35 40 45
 Thr Cys Val Pro Gln Pro Gln Ile Thr Val Gln Phe Asn Asp Val His
 50 55 60
 Ser Ile Gln Phe Pro Glu Ser Ile Gly Asn Cys Cys Asn Ser Ile Ser
 65 70 75 80
 Ser Met Pro Ile Asn Ser Pro Arg Pro Thr Ser Pro Trp Pro Pro Leu
 85 90 95
 Pro Leu Leu Ile Cys Glu Leu Pro Lys Pro Leu Pro Leu Pro Ala Phe
 100 105 110
 Asp Trp Leu
 115

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1046 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGGCTTAGTT AGGAGCTATG GCTAAACATC ATCCTGATTT GATCTTTTGC CGCAAGCAGG 60
CTGGTGTGTC CATCGGAAGA CTGTGTGAAA AATGTGATGG CAAGTGTGTG ATTTGTGACT 120
CCTATGTGCG TCCCTGCACT CTGGTGCGCA TATGTGATGA GTGTAACATAT GGATCTTACC 180
AGGGGCGCTG TGTGATCTGT GGAGGACCTG GGGTCTCTGA TGCCTATTAT TGTAAGGAGT 240
GCACCATCCA GGAGAAGGAC AGAGATGGCT GCCCAAAGAT TGTCAATCTG GGGAGCTCTA 300
AGACAGACCT CTTCTATGAA CGCAAAAAAT ACGGCTTCAA GAAGARGTGA TTGGTGGGTG 360
GCCCCCTTCCT CCCCCCAACA TCAGTCTGCT GCAGCTGCCA GAAAACATGC CTACTACTAC 420
CAGCAGAAAAG GGAGCAGAGC CCAGAGCATC ACCAGGAGTG CCTGCTAGTG TACTGGCAGC 480
TTGCCACCCC CTCCTCTCCC TTCACCCAGA CACGTGGTAG GGATGGAAAA GGATTCTTCA 540
CAGAGCACTC TGGCACACCA TATCGGAGAA AACTTGATAG ATTAGTTAAT GGTTTTTTCTT 600
GAATTCGAGA AGCATAGATC TGTCTCCAT ATTGGTATGT TCTCCCTCAA CCAAGATCTT 660
CTAAAAAGAA ATAATATTTT AGTCTTCTGC TTGAGGAACT GACTGTGAAG CGACGCCCAG 720
TGAAAAACAT GTTCTTGAG CAGCTCTGGT GGCAGCTGTC CTTGAGGAAC CTTTGGTGTG 780
TGGTGGGAAG CTATCAGAAC AAGAAATGTA GGCATTTCCC GTTTTTTTGG GGGGGGGGGG 840
TGGGGGGGCA GGGCTCTGCC CTCTTGAAAG GCATTTACTT GTTTAACACT TGTCCAGCTA 900
CAGTGGGGTA CAGTAGCTGG CTATTCACAG GCATCATCAT AGCCCACTAG TCTCATATTA 960
TTTTCTTTT GAGAAATTGG AACTCTTTC TGTGCTATT ATATTAATAA AGTTGGTGTT 1020
TATTTTCTGG TAAAAA AAAA 1046

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

CCTAAAGGAC TCCGACYTCC TGC ACTGGAA ACACAGCCTG TCAGAGCTCA TCGATATCAG	660
CATCGCACAG AAAACGGCCA TCTGGAGGCT GTATGGCCGC AGCACCATGG CACTGCAACA	720
GGCCCAGATG TTGCTGAGCA TGAACAGCCT GGAGGCGGTG AATGCGGGCG TGCAGCAGAA	780
CAACACAGAG TCCTTTGCTG TCGCACTCTG CCACCTCGCA GAGCTACACG CGGAGCAGGG	840
CTGTTTTGCT GCAGCTTCTG AAGTGTTAAA GCACTTGAAG GAACGATTTC CGCCTAATAG	900
TCAGCACGCC CAGTTATGGA TGCTATGTGA TCAAAAATA CAGTTTGACA GAGCAATGAA	960
TGATGGCAAA TATCATTTGG CTGATTCCT TGTACAGGA ATCACAGCTC TCAATAGCAT	1020
AGAGGGTGTT TATAGGAAAG CGGTTGTATT ACAAGCTCAG AACCAAATGT CAGAGGCACA	1080
TAAGCTTTTA CAAAATTGT TGGTTCATTG TCAGAACTG AAGAACACAG AAATGGTGAT	1140
CAGTGTCCTA CTGTCCGTGG CAGAGCTGTA CTGGCGATCT TCCTCCCCTA CCATCGCGCT	1200
GCCCATGCTC CTGCAGGCTC TGGCCCTCTC CAAGGAGTAC CGGTTACAGT ACTTGGCCTC	1260
TGAAACAGTG CTGAACTTGG CTTTTCGCA GCTCATTCTT GGAATCCCAG AACAGGCCTT	1320
AAGTCTTCTC CACATGGCCA TCGAGCCCAT CTTGGCTGAC GGGGCTATCC TGGACAAAGG	1380
TCGTGCCATG TTCTTAGTGG CCAAGTGCCA GGTGGCTTCA GCAGCTTCCT ACGATCAGCC	1440
GAAGAAAGCA GAAGCTCTGG AGGCTGCCAT CGAGAACCTC AATGAAGCCA AGAACTATTT	1500
TGCAAAGGTT GACTGCAAAG AGCGCATCAG GGACGTCGTT TACTTCCAGG CCAGACTCTA	1560
CCATACCCTG GGGAAGACCC AGGAGAGGAA CCGGTGTGCG ATGCTCTTCC GGCAGCTGCA	1620
TCAGGAGCTG CCCTCTCATG GGGTACCCTT GATAAACCAT CTCTAGAGAG GACATCCCTG	1680
CTGGGCTGCT GTGCAGAGTA TAAGATTTTG GACTTGTTCA TGTCCCCTCT CTCCCTATAA	1740
ATGATGTATT TGTGACACCC TATCTTGTCATAAACAGCA TTCTGATTAG TTTGTCTTAA	1800
AAAAAAAAAA AAAA	1814

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Asp Ala Leu Lys Asp Ser Asp Xaa Leu His Trp Lys His Ser Leu

1	5	10	15
Ser Glu Leu Ile Asp Ile Ser Ile Ala Gln Lys Thr Ala Ile Trp Arg	20	25	30
Leu Tyr Gly Arg Ser Thr Met Ala Leu Gln Gln Ala Gln Met Leu Leu	35	40	45
Ser Met Asn Ser Leu Glu Ala Val Asn Ala Gly Val Gln Gln Asn Asn	50	55	60
Thr Glu Ser Phe Ala Val Ala Leu Cys His Leu Ala Glu Leu His Ala	65	70	75
Glu Gln Gly Cys Phe Ala Ala Ala Ser Glu Val Leu Lys His Leu Lys	85	90	95
Glu Arg Phe Pro Pro Asn Ser Gln His Ala Gln Leu Trp Met Leu Cys	100	105	110
Asp Gln Lys Ile Gln Phe Asp Arg Ala Met Asn Asp Gly Lys Tyr His	115	120	125
Leu Ala Asp Ser Leu Val Thr Gly Ile Thr Ala Leu Asn Ser Ile Glu	130	135	140
Gly Val Tyr Arg Lys Ala Val Val Leu Gln Ala Gln Asn Gln Met Ser	145	150	155
Glu Ala His Lys Leu Leu Gln Lys Leu Leu Val His Cys Gln Lys Leu	165	170	175
Lys Asn Thr Glu Met Val Ile Ser Val Leu Leu Ser Val Ala Glu Leu	180	185	190
Tyr Trp Arg Ser Ser Ser Pro Thr Ile Ala Leu Pro Met Leu Leu Gln	195	200	205
Ala Leu Ala Leu Ser Lys Glu Tyr Arg Leu Gln Tyr Leu Ala Ser Glu	210	215	220
Thr Val Leu Asn Leu Ala Phe Ala Gln Leu Ile Leu Gly Ile Pro Glu	225	230	235
Gln Ala Leu Ser Leu Leu His Met Ala Ile Glu Pro Ile Leu Ala Asp	245	250	255
Gly Ala Ile Leu Asp Lys Gly Arg Ala Met Phe Leu Val Ala Lys Cys	260	265	270
Gln Val Ala Ser Ala Ala Ser Tyr Asp Gln Pro Lys Lys Ala Glu Ala	275	280	285
Leu Glu Ala Ala Ile Glu Asn Leu Asn Glu Ala Lys Asn Tyr Phe Ala	290	295	300
Lys Val Asp Cys Lys Glu Arg Ile Arg Asp Val Val Tyr Phe Gln Ala			

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:51:

- 51 -

AAACAACCTG TCCTGTTTTG TCAGTTCCCA GCTTCTTCGT TTAGAATAAA TTAGACCAAA 1020
 AGAAGAAACG TGCTTGCTCTC TGTATACCCG CAGAATGAAG TTACTGTTGT TAAAACCGGA 1080
 TTTTTTCATT TTACTAGGTT CCGAAGAGTC CAGATGCTTG GTAGATGTTC AATACGTGAT 1140
 TTTTTTTTTA ATTGAATGTG TTCATTTAAA ATCCTCCTTA ACATTTCTAG AAAGACTTCT 1200
 TTCAATAAAT AATGGAATCT TAGAGGAAAA GTGGTTTTTTT AAAAGCTAGG GAACTCCTCC 1260
 ACTAAAAGTA ACCATTGGAA ACCTCGAATG AGGGCTAAAAG TTTTAATCAT AAGAGAAAAG 1320
 GCAGCATAAT GAAATGTGTA CACATACATA GTCAGTGGTC CATTTTAGGA AGCCAGTGGC 1380
 GTCTGATAAA GAAATGTTAA GAGTAGTGAG GTTGAGGAAG GAAATTGTGG GGATTTGAAA 1440
 TATTCTCTTT ATGTTGTTTC TCTTCTGAGT CATGGTAAAA CAATAAATTA TCATCTCTAG 1500
 GTGGCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1540

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Leu Leu Leu Lys Pro Asp Phe Phe Ile Leu Leu Gly Ser
 1 5 10 15
 Glu Glu Ser Arg Cys Leu Val Asp Val Gln Tyr Val Ile Phe Phe Leu
 20 25 30
 Ile Glu Cys Val His Leu Lys Ser Ser Leu Thr Phe Leu Glu Arg Leu
 35 40 45
 Leu Ser Ile Asn Asn Gly Ile Leu Glu Glu Lys Trp Phe Phe Lys Ser
 50 55 60

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ANTGACGCCTT TAGCTAGTCC TTCTATCA

29

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TNCAACAGTAT CAACCAGAAG TGCCAATC

29

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GNAAACAGTAT TAAATTGCAG AGTTCCAG

29

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CNAATCATCAT CTCGCTTACA CAGTCAGG

29

- (2) INFORMATION FOR SEQ ID NO:57:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ANCGAGACAGA CCAAGGCTCA CAGGTGAA

29

- (2) INFORMATION FOR SEQ ID NO:58:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GNGGACACACA CTCATAAAAC AGAAAATA

29

- (2) INFORMATION FOR SEQ ID NO:59:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ANTAACCATAG AGTTTGGCTG GAGACCAC

29

- (2) INFORMATION FOR SEQ ID NO:60:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ANTCTTCCGAT GGCAACACCA GCCTGCTT

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GNTCACCATTT CTGTGTTCTT CAGTTTCT

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ANATTTAGGCT TATGCTGACC TCGTTGTA

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met	Gly	Asn	Ala	Ser	Tyr	Ser	Asp	Ser	Tyr	Leu	Glu	Gly	Ile	Leu	Leu	1	5	10	15
Lys	Gly	Val	Phe	Thr	Cys	Glu	Pro	Trp	Ser	Val	Ser	Val	Gly	Trp	Ser	20	25	30	
Thr	Ser	Val	Asp	Cys	Gly	Trp	Phe	Gln	Ser	Ala	Trp	Leu	Arg	Ser	Ser	35	40	45	
Thr	Glu	Gly	Ser	Thr	Gly	Ala	Ala	Leu	Trp	Gln	Arg	Leu	Arg	Arg	Glu	50	55	60	
Met	Asp	Gln	Pro	Thr	Pro	Gly	Thr	Trp	Leu	His	Gly	Ile	Arg	Lys	Gly	65	70	75	80
Arg	Cys	Trp	Pro	Leu	Cys	Ser	Cys	Cys	Leu	Phe	Leu	Phe	Leu	Phe	Ala	85	90	95	
Phe	Asp	Leu	Val	Ala	Thr	Asp	Arg	Val	Ala	Arg	Asp	Leu	Val	Phe	Ser	100	105	110	
Ser	Arg	His	Pro	Ser	Thr	Pro	Ala	Leu	Ser	Gln	Val	Ser	Cys	Cys	His	115	120	125	
Ala	Asn	Ala	Met	Ser	Thr	Leu	Ala	Pro	Arg	Pro	Lys	Ser	Val	Gln	Arg	130	135	140	
Trp	Pro	Thr	Xaa	Ser	Ser	His	Tyr	Ser	Leu	Asn	Ser	Met	Tyr	His	Leu	145	150	155	160
Pro Leu																			

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu	Val	Gly	Gly	Pro	Phe	Leu	Pro	Pro	Thr	Ser	Val	Cys	Cys	Ser	Cys	1	5	10	15
Gln	Lys	Thr	Cys	Leu	Leu	Leu	Pro	Ala	Glu	Arg	Glu	Gln	Ser	Pro	Glu	20	25	30	

His His Gln Glu Cys Leu Leu Val Tyr Trp Gln Leu Ala Thr Pro Ser
35 40 45

Ser Pro Phe Thr Gln Thr Arg Gly Arg Asp Gly Lys Gly Phe Phe Thr
50 55 60

Glu His Ser Gly Thr Pro Tyr Arg Arg Lys Leu Asp Arg Leu Val Asn
65 70 75 80

Gly Phe Ser

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTAACCTTCT TCTGCGCGGC TGCAGCTCGG GACTTCGGCC TGACCCAGCC CCCATGGCTT	60
CAGAAGAGCT ACAGAAAGAT CTAGAAGAGG TAAAGGTGTT GCTGGAAAAG GCTACTAGGA	120
AAAGAGTACG TGATGCCCTT ACAGCTGAAA AATCCAAGAT TGAGACAGAA ATCAAGAACA	180
AGATGCAACA GAAATCACAG AAGAAAGCAG AACTTCTTGA TAATGAAAAA CCAGCTGCTG	240
TGGTTGCTCC CATAACAACG GGCTATACGG TGAAAATCAG TAATTATGGA TGGGATCAGT	300
CAGATAAGTT TGTGAAAATC TACATTACCT TAACTGGAGT TCATCAAGTT CCCACTGAGA	360
ATGTGCAGGT GCATTTTACA GAGAGGTCAT TTGATCTTTT GGTAAAGAAT CTAAATGGGA	420
AGAGTTACTC CATGATTGTG AACAACTCTCT TGAAACCCAT CTCTGTGGAA GGCAGTTCAA	480
AAAAAGTCAA GACTGATACA GTTCTTATAT TGTGTAGAAA GAAAGTGGAA AACACAAGGT	540
GGGATTACCT GACCCAGGTT GAAAAGGAGT GCAAAGAAAA AGAGAAGCCC TCCTATGACA	600
CTGAAACAGA TCCTAGTGAG GGATTGATGA ATGTTCTAAA GAAAATTTAT GAAGATGGAG	660
ACGATGATAT GAAGCGAACC ATTAATAAAG CCTGGGTGGA ATCAAGAGAG AAGCAAGCCA	720
AAGGAGACAC GGAATTTTGA GACTTTAAAG TCGTTTTGGG AACTGTGATG TGATGTGGAA	780
ATACTGATGT TTCCAGTAAG GGAATATTGG TGAGCTGCAT ATATAAATTT GACAGATAGC	840
TATTTACATA GCCTTCTAAG TAAAGGCAAT GAATTCTCCA TTTCCTACTG GAGGATTTAT	900
TTAAATAAAA TATGCTTATT AAACACTCCT GCAAAGATGG TTTTATTAGT ACCCTGGTCA	960

TTTTGTTCAA GGAAGGGTTA TATTGCATTC TCACGTGAAA TATAAAAAGC AAGTCTTGCC 1020
 CAATAAAAC GCTACATTGT GTGTATTTTT TGTTCAGCTA AGAATTGGAA AAGTATTTGC 1080
 TTGCCTTTTA AGTTACTGAC ATCAGCTTCC ACCAGTGTA AAATTGAGTA AAACCTGAAG 1140
 TTTTGCATAA AATGCAAATC GGTGCCTGTG CTTGAAGGTT GCTGTAGAGC ATCTGACCCC 1200
 TTATTACCAC CTTAAGCAAT GTATATGCCA TGCATTACCA TGCAC⁴TAATT CAATCACAGG 1260
 TGTTTCTATC TAGATTTAAA TATATTTGTC AATGAATGTG GAATAGAAAA TCTAAACATG 1320
 ACAATAATAG ACATATCTTT GTATGGTACC AGTTAGTTTT GCCGTGGATC AGATGGTTTA 1380
 TAAAAGTAAT AACCATAAAG CAAAAAATAA TTTGAAAGCC CGTCTATTCC TATGCTCAAT 1440
 AAAGTTAAGT TTTTTTCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500
 AAAAAAAAAA AAAAAAAAAA A 1521

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Ala	Ser	Glu	Glu	Leu	Gln	Lys	Asp	Leu	Glu	Glu	Val	Lys	Val	Leu
1				5				10					15		
Leu	Glu	Lys	Ala	Thr	Arg	Lys	Arg	Val	Arg	Asp	Ala	Leu	Thr	Ala	Glu
			20				25					30			
Lys	Ser	Lys	Ile	Glu	Thr	Glu	Ile	Lys	Asn	Lys	Met	Gln	Gln	Lys	Ser
		35				40					45				
Gln	Lys	Lys	Ala	Glu	Leu	Leu	Asp	Asn	Glu	Lys	Pro	Ala	Ala	Val	Val
	50				55				60						
Ala	Pro	Ile	Thr	Thr	Gly	Tyr	Thr	Val	Lys	Ile	Ser	Asn	Tyr	Gly	Trp
65				70				75						80	
Asp	Gln	Ser	Asp	Lys	Phe	Val	Lys	Ile	Tyr	Ile	Thr	Leu	Thr	Gly	Val
			85				90					95			
His	Gln	Val	Pro	Thr	Glu	Asn	Val	Gln	Val	His	Phe	Thr	Glu	Arg	Ser
			100				105						110		

Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Ser Tyr Ser Met Ile
115 120 125

Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Gly Ser Ser Lys Lys
130 135 140

Val Lys Thr Asp Thr Val Leu Ile Leu Cys Arg Lys Lys Val Glu Asn
145 150 155 160

Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu Lys
165 170 175

Glu Lys Pro Ser Tyr Asp Thr Glu Thr Asp Pro Ser Glu Gly Leu Met
180 185 190

Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Asp Met Lys Arg
195 200 205

Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Lys Gly
210 215 220

Asp Thr Glu Phe
225

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TGCGTCATGC AGTGCGCCGG AGGAACTGTG CTCTTTGAGG CCGACGCTAG GGGCCCGGAA	60
GGGAAACTGC GAGGCGAAGG TGACCGGGGA CCGAGCATTT CAGATCTGCT CGGTAGACCT	120
GGTGCACCAC CACCATGTTG GCTGCAAGGC TGGTGTGTCT CCGGACACTA CCTTCTAGGG	180
TTTTCACCC AGCTTTCACC AAGGCCTCCC CTGTTGTGAA GAATTCCATC ACGAAGAATC	240
AATGGCTGTT AACACCTAGC AGGGAATATG CCACCAAAAC AAGAATTGGG ATCCGGCGTG	300
GGAGAACTGG CCAAGAACTC AAAGAGGCAG CATTGGAACC ATCGATGGAA AAAATATTTA	360
AAATTGATCA GATGGGAAGA TGGTTTGTG CTGGAGGGGC TGCTGTTGGT CTTGGAGCAT	420
TGTGCTACTA TGGCTTGGGA CTGTCTAATG AGATTGGAGC TATTGAAAAG GCTGTAATTT	480
GGCCTCAGTA TGTCAAGGAT AGAATTCATT CCACCTATAT GTACTTAGCA GGGAGTATTG	540
GTTTAACAGC TTTGTCTGCC ATAGCAATCA GCAGAACGCC TGTTCATG AACTTCATGA	600

TGAGAGGCTC TTGGGTGACA ATTGGTGTGA CCTTTGCAGC CATGGTTGGA GCTGGAATGC 660
 TGGTACGATC AATACCATAT GACCAGAGCC CAGGCCCAAA GCATCTTGCT TGGTTGCTAC 720
 ATTCTGGTGT GATGGGTGCA GTGGTGGCTC CTCTGACAAT ATTAGGGGGT CCTCTTCTCA 780
 TCAGAGCTGC ATGGTACACA GCTGGCATTG TGGGAGGCCT CTCCACTGTG GCCATGTGTG 840
 CGCCCAGTGA AAAGTTTCTG AACATGGGTG CACCCCTGGG AGTGGGCCTG GGTCTCGTCT 900
 TTGTGTCTC ATTGGGATCT ATGTTTCTTC CACCTACCAC CGTGGCTGGT GCCACTCTTT 960
 ACTCAGTGGC AATGTACGGT GGATTAGTTC TTTTCAGCAT GTTCCTTCTG TATGATACCC 1020
 AGAAAGTAAT CAAGCGTGCA GAAGTATCAC CAATGTATGG AGTTCAAAAA TATGATCCCA 1080
 TTAACGAT GCTGAGTATC TACATGGATA CATTAAATAT ATTTATGCGA GTTGCAACTA 1140
 TGCTGGCAAC TGGAGGCAAC AGAAAGAAAT GAAGTGACTC AGCTTCTGGC TTCTCTGCTA 1200
 CATCAAATAT CTTGTTTAAT GGGGCAGATA TGCATTAAAT AGTTTGTACA AGCAGCTTTC 1260
 GTTGAAGTTT AGAAGATAAG AAACATGTCA TCATATTTAA ATGTTCCGGT AATGTGATGC 1320
 CTCAGGTCTG CCTTTTTTTC TGGAGAATAA ATGCAGTAAT CCTCTCCCAA ATAAGCACAA 1380
 AAAAAAAAAA AAAA 1394

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val
 1 5 10 15
 Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile
 20 25 30
 Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys
 35 40 45
 Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu
 50 55 60
 Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln Met

65	70	75	80
Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu	85	90	95
Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys	100	105	110
Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr	115	120	125
Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala	130	135	140
Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp	145	150	155
Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu	165	170	175
Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala	180	185	190
Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr	195	200	205
Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly	210	215	220
Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys	225	230	235
Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe	245	250	255
Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly	260	265	270
Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser	275	280	285
Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val	290	295	300
Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu	305	310	315
Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met	325	330	335
Leu Ala Thr Gly Gly Asn Arg Lys Lys	340	345	

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCTTTTTTTT	TTTTTTTGG	TTGAGATGGG	GTCTCGCCAT	GTTTCCCACA	CTGATCTTGA	60
ACTCCTGGGC	TCCAGGAATT	CTCCTACTTT	GGCCTCCCAA	AGTGTGGGA	ATATTGGCAT	120
GAACCACAGC	ACCTGACTTG	CATATTTGTG	AATTCCCCAA	ATTGCTTTTT	TTAAATTGAT	180
TTCTAATTTT	ATTTTCATTG	TATGGGGAAC	ATACTTTGTA	TGGTTTCAAT	GTTTTAAAAT	240
TAATTGAGAC	TTGTTTTATG	ACTTAGCATA	TGGTCTGTGT	TGAAGAAGGC	TCCATGTACA	300
CTTGAGAATA	ATATGTATAC	TGTGGTTGTT	GGGTGGATTT	TCTATGTATG	TTTARGTGAT	360
ATGGTTTTAT	AGTGTGTGTT	AARTCTTCTA	TTTTCTTCTT	TTTCTGCCCA	GTTTTATTTT	420
TGAAAGCATA	CTGARGTCTC	CAACTCARTG	CCTTAGCCTC	CTGAGCAGTT	GGGACTACAG	480
GCATACGCCA	CTACACCCAG	CAATTTTTTT	GTATTTTTCT	GTAAGACAG	AGTTTCACCA	540
TGTTGCCTAG	GCTGGTCTCA	GATTCCTGGA	CTCAAGTGAT	CTCGATTCCC	GGCCTCTGCC	600
TCCCGGGGTG	CTGGGATTGC	AGGCATGAGC	TACTATGCCT	GGCAAATTTT	ATTTTTCTTT	660
TTATTTTGTC	ACATAATTAA	AGCTACTCCA	GAATCCCTT	GATTTCTGCT	TGCCTGGTAT	720
ATCTTTTTTC	CATTTTTTAA	CTGTCAGCCT	TTTTTG TGCC	TGTTAATCTA	AAGTATGTGT	780
TTCGTAGATA	ATATGTAGCT	GGATCATATT	TTAAAAATAT	TTATTC TGCC	AAGCTCTGTC	840
TTTTGATTGG	AGTATTCTTT	CATTTATGTT	TGTAATTACT	GATGAGGGGG	GACTAATGT	900
CTGCTGTTTT	GCTATTTGTT	TCCCATGTC	TTATGTCTTC	ATTACTGACT	TTTTTATTAA	960
ACAAC TATT	TCTTGGGTAC	CATTTTAAGT	CCCTCTCCCA	CTCATTTTTT	AATGTTTTTT	1020
TGTGTTTACT	TTTGTTTTTA	TTGTTTGCCC	TGATATTAAA	ATTAACATTT	TACCTTGAAA	1080
TAGTTGGCTT	CAGATTAATA	TCAACTTAGT	TTCAATAGCA	TAGGAAATTT	GCTTCACTAT	1140
ATTTCCATTT	TCTCCCGTTC	CTTTGTGCTA	TTATTACTAT	ACCAATTAGA	TCTCTACACA	1200
ATATAGGCAT	ATCAACACAT	TTTGTAATTA	TTTCCTTATC	CAGTTGTCTT	TTAATATAGA	1260
TCTGTGAAGA	AAAGTATTAC	ACAAATAGAT	CTATTCTGTT	TTTTATAATT	ATTTAATTAC	1320
CTTTGGTGGT	GCTGTTTATT	TTTCATGCAT	TTGAGTTACT	GTCTAGTATT	CATTCATTTT	1380
TCTCTGAATC	ACTCCCTTTA	GTATTGCTTG	TAGGGCAGGT	CTGCTAGCAT	TGAATTCCTT	1440

TAATTTTGT GACTCTGCAA ATGCCATAAT TTCTCTTTTG TTTGTGAAGG ATAGTTTTC 1500
TAGATACAGA ATTTGCAGTT GGCATTCTTT TTTACTTTAGC AGTTTGAAAA TATTTCCCAT 1560
TGTTGGCCGG GCACAGTGGC TCACGCCTGT GGTCTAGCA CTTTGGGAGG CCGAGGCGGG 1620
CGGATCGTCT GGGGTCGGGA GTTCGGGACC GGCCTGGCCA ATATGGTGAG GCCCTGTTTC 1680
TGCTAAAATA TAAAAATTGG CTGGGCATGA TGGCGGGTGC CTCTAGTCCC AGCTGCTCGG 1740
GAGGCTGAGG TGGGGGAGTC GCTTGAGCCC GGGAGATGAT GGCTGTGGTG AGCCGGGATG 1800
GCGCCGCTGC ACTCCGGCCT GGGCGGCTGA GTGAGACTCC ATCCCCGAAA AAAAAAAAAA 1860
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 1908

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Arg	Gly	Ala	Leu	Met	Ser	Ala	Val	Leu	Leu	Phe	Val	Ser	Pro	Cys
1				5					10					15	
Leu	Met	Ser	Ser	Leu	Leu	Thr	Phe	Leu	Leu	Asn	Asn	Tyr	Phe	Leu	Gly
			20					25					30		
Tyr	His	Phe	Lys	Ser	Leu	Ser	His	Ser	Phe	Phe	Asn	Val	Phe	Leu	Cys
		35					40					45			
Leu	Leu	Leu	Phe	Leu	Leu	Phe	Ala	Leu	Ile	Leu	Lys	Leu	Thr	Phe	Tyr
	50					55					60				
Leu	Glu	Ile	Val	Gly	Phe	Arg	Leu	Ile	Ser	Thr					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3076 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTTTTTTTTT TTTTTC AAT TTCATTTAGT TCTGCCCTGA TCTTGGTTAT TTCCTTTTTT 60
TCTGCTGGGT TTGGGTTTGG TTTGTTCTTA TTTCTCTAGT TCCTTGAGGT GTGACCTTAR 120
AATGTCAATT TGTGCTCTTT CAATCTTTTT GATGTAGGCG TTGAGGGCTG TGGACTTTTC 180
TCTTGGCACT CCCTTTGGTG TATCCCARAG GTTTTGATAG GTTGTGTCAT TATTGCAATT 240
CAGTTTGAAG AATTTCTTAA TCTCCACCTT GATTTTGTTT TTGACCCAAT GCTCATTCAG 300
GAGCAGGTTA TTTACTTTCC ATGTA CTGCTTGA AGCTTCCTTT TGGAGTTGAT 360
TTCCAGTTTT ATTCCACTGT GATTTGAGAG AGTGCTTTAC ATAATTTCAA TTTTCTTAAT 420
TTTATTAAGG CTCGTTTTAT GGCCTATAAT ATGGTCTATC TTGGAGAAAAG TTCCATGCAC 480
TG TAGAATAG AATGTGTATT CTGTGGTTGT TGGATGAAAT GTTCTGCATA TATTCCTAGA 540
TTGCCTCCCC ACAAAGGTT GCATCAATGT CTGTGTTTCT CTACACCATC TCACCCTTGC 600
CAACTTCGGG TTTTCATCAGA CCTTACTGAT TGTCAGTATG ATCTGTGAAA CAAATCTCTC 660
AGTTTTGATT TGCATTTTTT AAATTATGAG AGCTTGAACA CCATTTTACA TGTTTATTGG 720
CTGTTGTTAT TTCCTTTTTG AGATCTGTTC GTTATATGCT TTGCCCCTTT TTCTGTTGGG 780
TGGTTATTAT TTTTCTTATT GAATGGTATA AGCTCTTTGT AAGTTAAGGA CATTAGCCCT 840
TAGTCAGATA TTTTGACTTA GGTTTTAATT TTTTCCACA CAGAAGTTTT AAGCTCTGTG 900
GCAAATTTAT CAGTCTTATA TCACTACAGG GTTATAAATA TTAGYTATCA CTTCCGGGTTT 960
GTGTCTTGCT TAGAAAGCMT CATTTGAAGA TTGTAAATGT TAGTAAGTTT CCCCATATTT 1020
TCCTCTAGGA CTTCCATGGT TTAATTTGTT TTGTTTAAAY TAGGAATTGG CATTACATC 1080
CTYTTTTGTC CCAGGTCTCA GAGGTCCCTT GTATCTTATA GAGCAGTATT GTTTTATGTT 1140
ATTTTCCCAT GTATAATTTA AAAACAAAAT ACGTTGTTCA AAACAAAATA CAGTGGCAGC 1200
AGATAATGGC AGTATCTCTG TAACTGCTGG TAAACTGTAT TTCATAGTGA AGTGTTTATA 1260
AACTAAAGAG TCATTGATTT GGTTCCTGG CTAATTAATA TCTGAATTCC ATTTGAAGTT 1320
CCATTGAAAT CATGGTTTTA CTCTATAGCA GTGGATGTTT TTTCCCAACC TTTCTGATAT 1380
TTTTTTCCTT CCTGAGACAG GGTCTTGCTC TGTCACCTGG GATGGAGTGT AGTTGCACCA 1440
TCAAGGCTTA CTGCAGTCTC AACTCTCTGA GCTCAAGTGA TCCTGCCACC TCAGCCTCTT 1500
GAGTAGCAAG GATTACAGGC ACCTACCACT ATGCCTGGCT AATTTTATA TTTTGTAG 1560
AGATGGATTC TCACTATGTT GCGCGGGCTC ATCTTGAAC TCGAGCTCAAG CAATCTGTCC 1620

ATCTTGGCCT CCCAAAGTGC TGGGATTATA GCGTGAGCC ACTGCACCTG GCCCCTTTCT	1680
GATTATTTTA ATCTATCTTT AAATGTTCAA AGTGATTGTC CTAATTCATT TAAAGCATAT	1740
TTAGTTTTTT TTAAATTGAG TGTATTTTAT CTAGATATTT TTAAAAGGCA GCATCTAACC	1800
TTGGATTTTA TAAATACATC TAAATTTGTT ATTTCCAGAA TGCTTCAAAA CAGATCTCTG	1860
TAGCCTCGTG CTTTGTTATT GTTAGGTTTT TTTTTTTTGT TTTGAGACAG GGTCTTGCTC	1920
TATCTGGAGT GCAGTGGCAC AGTCATAGCT CACTGTACCC TCAAACCTCT AAACCTCAAGT	1980
AATCCTCCCA TCTCAGCCTC CTGAGTAGTT GGGACCACAG TCATGCACCA GCATGCCTGG	2040
CTAATTTTTT AAATTTTGTT CTTAATAGAG ACAGAGTCTT GCTGTGTTGT TCAGGCTGGT	2100
CTCAAACCTC TGGGCTCAAG CGATCCTCCC ACCTCAGCCT CCTAAAGTGC TGAGATTACG	2160
GATGTGAATC ATTACACCCA GCCTATTAAT GGTTTTGTAT AGCAAGTCTT TTGTGGGTGG	2220
TGGAAAGATG AAGTGCTGTG AAATATTGTA GGAGCAGAAA CTTGAAATGT GGCAAAAACC	2280
ACATGGGCAA AATTTCTGTC TCTTTTCTTA TTTTGTCTTT TTTGTTTAAA GGTTTTCTA	2340
TTGGGAAAGC TACTGATCGG ATGGATGCTT TCAGGAAAGC AAAGAACAGA GCAGTTCACC	2400
ATTTGCATTA TATAGAACGA TATGAAGACC ATACAATATT CCATGATATT TCATTAAGAT	2460
TTAAAAGGAC GCATATCAAG ATGAAGAAAC AACCCTAAAG TTACGGCCTC CGCTGCCACA	2520
GGGCCATCAT CACCATCTGC CGGCTCATTG GCATCAAAGA CATGTATGCC AAGGTCTCTG	2580
GGTCCATTAA TATGCTCAGC CTCACCCAGG GCCTCTTCCG TGGGCTCTCC AGACAGGAAA	2640
CCCATCAACA GCTGGCTGAT AAGAAGGGCC TCCATGTTGT GGAAATCCGG GAGGAATGTG	2700
GCCCTCTGCC CATTGTGGTT GCGTCCCCC GGGGGCCCTT GAGGAAGGAT CCAGAGCCAG	2760
AAGATGAGGT TCCAGACGTC AAACCTGGACT GGAAGATGT GAAGACTGCA CAGGGAATGA	2820
AGCGCTCTGT GTGGTCTAAT TTGAAGAGAG CCGCCACGTA ACCTCTCTGG CCTTGTGCAG	2880
CCAGTTCCTG TGCTGCCCTG CACCTAGGAG AGACTCAGCC CCTCACAGCT TGGGATGTTA	2940
CCTTGCCTTT TGTTTGTTTT GAGGGAAGTT TAATCTTTAA ACTCTTTGGA AATAAATAAT	3000
TATAGCTTTC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3060
AAAAAAAAAA AAAAAA	3076

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	Gly	Lys	Ile	Ser	Val	Ser	Phe	Leu	Ile	Phe	Ala	Phe	Leu	Phe	Lys	1	5	10	15
Gly	Phe	Ser	Ile	Gly	Lys	Ala	Thr	Asp	Arg	Met	Asp	Ala	Phe	Arg	Lys	20	25	30	
Ala	Lys	Asn	Arg	Ala	Val	His	His	Leu	His	Tyr	Ile	Glu	Arg	Tyr	Glu	35	40	45	
Asp	His	Thr	Ile	Phe	His	Asp	Ile	Ser	Leu	Arg	Phe	Lys	Arg	Thr	His	50	55	60	
Ile	Lys	Met	Lys	Lys	Gln	Pro	Lys	Gly	Tyr	Gly	Leu	Arg	Cys	His	Arg	65	70	75	80
Ala	Ile	Ile	Thr	Ile	Cys	Arg	Leu	Ile	Gly	Ile	Lys	Asp	Met	Tyr	Ala	85	90	95	
Lys	Val	Ser	Gly	Ser	Ile	Asn	Met	Leu	Ser	Leu	Thr	Gln	Gly	Leu	Phe	100	105	110	
Arg	Gly	Leu	Ser	Arg	Gln	Glu	Thr	His	Gln	Gln	Leu	Ala	Asp	Lys	Lys	115	120	125	
Gly	Leu	His	Val	Val	Glu	Ile	Arg	Glu	Glu	Cys	Gly	Pro	Leu	Pro	Ile	130	135	140	
Val	Val	Ala	Ser	Pro	Arg	Gly	Pro	Leu	Arg	Lys	Asp	Pro	Glu	Pro	Glu	145	150	155	160
Asp	Glu	Val	Pro	Asp	Val	Lys	Leu	Asp	Trp	Glu	Asp	Val	Lys	Thr	Ala	165	170	175	
Gln	Gly	Met	Lys	Arg	Ser	Val	Trp	Ser	Asn	Leu	Lys	Arg	Ala	Ala	Thr	180	185	190	

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 683 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CGCCAAGTGC GCATGGGGAC GCTATAGCAA TTCGTTTGCT GTCCTTCCTC TCCTTCGAAG	60
ATGACAAGGC CTACCATCGT TTCTTCCTGC CTTTGGGCCG TCAGGCAGTT GGTGGGACC	120
CGCTCCAACC CTCGGTTCTT CCTGCAATAC AGTGGATACA ATTTGTCATG GCTACTCTGA	180
GTGTTATAGG TTCAAGTTCA CTTATTGCCT ATGCTGTATT CCATAATATA CAGAAATCTC	240
CAGAGATAAG ACCACTTTTT TATCTGAGCT TCTGTGACCT GCTCCTGGGA CTTTGCTGGC	300
TCACGGAGAC ACTTCTCTAT GGAGCTTCAG TAGCAAATAA GGACATCATC TGCTATAACC	360
TACAAGCAGT TGGACAGATA TTCTACATTT CCTCATTTCT CTACACCGTC AATTACATCT	420
GGTATTTGTA CACAGAGCTG AGGATGAAAC ACACCCAGAG TGGACAGAGC ACATCTCCAC	480
TGGTGATAGA TTATACTTGT CGAGTTGGTC AAATGGCCTT TGTTTTCTCA AGCCTGATAC	540
CTCTGCTATT GATGACACCT GTATTCTGTC TGGGAAATAC TAGTGAATGT TTCCAAAAC	600
TCAGTCAGAG CCACAAGTGT ATCTTGATGC ACTCACCACC ATCAGCCATG GCTGAACTTC	660
CACCTTCTGC CAACACATCT GTC	683

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met	Ala	Thr	Leu	Ser	Val	Ile	Gly	Ser	Ser	Ser	Leu	Ile	Ala	Tyr	Ala
1				5				10					15		
Val	Phe	His	Asn	Ile	Gln	Lys	Ser	Pro	Glu	Ile	Arg	Pro	Leu	Phe	Tyr
			20					25					30		
Leu	Ser	Phe	Cys	Asp	Leu	Leu	Leu	Gly	Leu	Cys	Trp	Leu	Thr	Glu	Thr
			35					40					45		
Leu	Leu	Tyr	Gly	Ala	Ser	Val	Ala	Asn	Lys	Asp	Ile	Ile	Cys	Tyr	Asn
			50					55					60		
Leu	Gln	Ala	Val	Gly	Gln	Ile	Phe	Tyr	Ile	Ser	Ser	Phe	Leu	Tyr	Thr
			65					70					75		80
Val	Asn	Tyr	Ile	Trp	Tyr	Leu	Tyr	Thr	Glu	Leu	Arg	Met	Lys	His	Thr

	85		90		95
Gln Ser Gly Gln Ser Thr Ser Pro Leu Val Ile Asp Tyr Thr Cys Arg					
	100		105		110
Val Gly Gln Met Ala Phe Val Phe Ser Ser Leu Ile Pro Leu Leu Leu					
	115		120		125
Met Thr Pro Val Phe Cys Leu Gly Asn Thr Ser Glu Cys Phe Gln Asn					
	130		135		140
Phe Ser Gln Ser His Lys Cys Ile Leu Met His Ser Pro Pro Ser Ala					
	145		150		155
					160
Met Ala Glu Leu Pro Pro Ser Ala Asn Thr Ser Val					
	165		170		

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATATGGCTGG ACGCAGCACA AATTCCACCA ACTAAAGCAG GAGGCTCGGC GTGATGCAGA	60
TACCCAGACA CCATTATTAT GCTCACAGAA GAGATTCTAT AGCAGGGGCT TAAATTCCT	120
GGAATCCACC CTGACTTTTC CTGCCAGTAC TTCTACCATT TTTTGAAACT ACAATACTGG	180
AACATCCAGG AACTGGAGTT ATTCTACGCT AATGGATTGG AAAGAATGTT GGGAAAGGAC	240
ATCTTAAATC TTTTCTAACT ATGCCCTAAA CTGCAGAACT CAAAGGAAAT ATAGTGCCAT	300
TGTTAGTAGT CATTCTAGAT GAATTGGGAG TATCTCTCCA GTTATTCCCA GATTCCTAG	360
TGATCCTTAA AGTCTCTATT CAGGGAGAGG AAGACACTTT CCATCTCAGA GATAGACTCG	420
TGTTACCTTG ATGGATATTG GATTTGTCTA AGTCTCTTCT AGAAAAAATA AATTCTAGAT	480
TATTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA	524

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCCCGCTACC GGGTTGCGGC CGGAAGCCGG GCGCCGCGGC TCTGCTTCCC TCGGGGATCT	60
GGCGACATGG CCAGAAAGGC TCTCAAGCTT GCTTCGTGGA CCAGCATGGC TCTTGCTGCC	120
TCTGGCATCT ACTTCTACAG TAACAAGTAC TTGGACCCTA ATGACTTTGG CGCTGTCAGG	180
GTGGGCAGAG CAGTTGCTAC GACGGCTGTC ATCAGTTACG ACTACCTCAC TTCCCTGAAG	240
AGTGTCCCTT ATGGCTCAGA GGAGTACTTG CAGCTGAGAT CTAAGGTGCA CCTTCGCTCT	300
GCCAGGCGTC TCTGTGAGCT CTGCTGTGCC AACCGGGGCA CCTTCATCAA GGTGGGCCAG	360
CACCTGGGGG CTCTGGACTA CCTGTTGCCA GAGGAGTACA CCAGCACGCT GAAGGTACTG	420
CACAGCCAGG CTCCACAGAG CAGCATGCAA GAGATCCGCC AGGTCATCCG AGAAGATCTG	480
GGCAAGGAGG TGCTCGTTCT GGCTGTGAAG CAGCTGTTCC CAGAGTTTGA GTTTATGTGG	540
CTTGTGGATG AAGCCAAGAA GAACCTGCCT TTGGAGCTGG ATTTCTCAA TGAAGGGAGG	600
AATGCTGAGA AGGTGTCCCA GATGCTCAGG CATTTTGA CTCTGAAGGT CCCCCGAATC	660
CACTGGGACC TGTCCACGGA GCGGGTCCTC CTGATGGAGT TTGTGGATGG CGGGCAGGTC	720
AATGACAGAG ACTACATGGA GAGGAACAAG ATCGACGTCA ATGAGGTGAG GTCAAGAGCT	780
CAGGGCTGCT GTGCCGGGGA ACGTGGGCTT GGTCAAGGCT GCCCAGGAAG TGCCTGTGTG	840
TCCAGATCTC ACGCCACCTG GGCAAGATGT ATAGTGAGAT GATCTTCGTC AATGGCTTCG	900
TGCACTGCGA TCCCCACCCC GGCAATGTAC TGGTGCGGAA GCACCCCGGC ACGGGAAAGG	960
CGGAGATTGT CCTGTTGGAC CATGGGCTTT ACCAGATGCT CACGGAAGAA TTCCGCCTGA	1020
ATTACTGCCA CCTCTGGCAG TCTCTGATCT GGA CTGACAG GAAGAGAGTG AAGGAGTACA	1080
GCCAGCGACT GGGAGCCGGG GATCTCTACC CCTTGTTTGC CTGCATGCTG ACGGCGCGAT	1140
CGTGGGACTC GGTCAACAGA GGCATCAGCC AAGCTCCCGT CACTGCCACT GAGGACTTAG	1200
AGATTGCGAA CAACGCGGCC AACTACCTCC CCCAGATCAG CCATCTCCTC AACCACGTGC	1260
CGCGCCAGAT GCTGCTCATC TTGAAGACCA ACGACCTGCT GCGTGGCATT GAGGCCGCCC	1320
TGGGCACCCG CGCCAGCGCC AGCTCCTTTC TCAACATGTC ACGTTGCTGC ATCAGAGCGC	1380
TAGCTGAGCA CAAGAAGAAG AATACCTGTT CATTCCTCAG AAGGACCCAG ATCTCTTTCA	1440
GCGAGGCCTT CAACTTATGG CAGATCAACC TCCATGAGCT CATCCTGCGT GTGAAGGGGT	1500
TGAAGCTGGC TGACCGGGTC TTGGCCCTAA TATGCTGGCT GTTCCCTGCT CCACTCTGAG	1560

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TGGAATTGCT CTCCCTGCCC CATTCTGGTG TCTTTCCACT CCTCAGCCCC TCATCTTGCC      1620
TCCACCCAGC TGCTCCATTT TTGCCACATC GTGGCCCGCA GCCCAGAGT CACTGTCCAT      1680
GTCACCATCC TCCTCCTCCT TTGGAATCCT CTCCGCACAC TGTGGCCCTT GTCTCAGGGC      1740
CCACAAGCTG AACTGTGGCA TAGCTCTCTC TTCTTCTCCA AGAAGACTCA GCAGCCTACA      1800
TTCCCATTC TGGTATGTGC CATTGGGTTG GATGTCCCCA CTAATTCCGT TAACCCTTCC      1860
CATTGTCAAG ATGTGCCACG GGTGCCACTG GGGGCACACT GAACTTGTAG GGAGTGTGAT      1920
TTTGTGGAG GTGCACATGG TCTCTGAATT TGACAGAGAA CACCTTCCCT TTCCTTGCCA      1980
TGTCACCCTC CAGAGGAAGT CACACCTCAG CGAGGTGGTT TGGCATCTGG GGCCAACTCC      2040
ATTACAGCTA TGAGCTCACT GCTGTCAGTG ACGTTTGGTG TTTTCTGTAC TGTGTTTCAA      2100
TAAAAACTCC TTCAAGGTTG CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      2160
AAAAAAAAAA A                                                              2171

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(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

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Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
1           5           10           15
Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn
20          25          30
Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
35          40          45
Ile Ser Tyr Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
50          55          60
Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
65          70          75          80
Arg Leu Cys Glu Leu Cys Cys Ala Asn Arg Gly Thr Phe Ile Lys Val
85          90          95
Gly Gln His Leu Gly Ala Leu Asp Tyr Leu Leu Pro Glu Glu Tyr Thr
100         105         110

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Ser Thr Leu Lys Val Leu His Ser Gln Ala Pro Gln Ser Ser Met Gln
115 120 125

Glu Ile Arg Gln Val Ile Arg Glu Asp Leu Gly Lys Glu Val Leu Val
130 135 140

Leu Ala Val Lys Gln Leu Phe Pro Glu Phe Glu Phe Met Trp Leu Val
145 150 155 160

Asp Glu Ala Lys Lys Asn Leu Pro Leu Glu Leu Asp Phe Leu Asn Glu
165 170 175

Gly Arg Asn Ala Glu Lys Val Ser Gln Met Leu Arg His Phe Asp Phe
180 185 190

Leu Lys Val Pro Arg Ile His Trp Asp Leu Ser Thr Glu Arg Val Leu
195 200 205

Leu Met Glu Phe Val Asp Gly Gly Gln Val Asn Asp Arg Asp Tyr Met
210 215 220

Glu Arg Asn Lys Ile Asp Val Asn Glu Val Arg Ser Arg Ala Gln Gly
225 230 235 240

Cys Cys Ala Gly Glu Arg Gly Leu Gly Gln Gly Cys Pro Gly Ser Ala
245 250 255

Cys Val Ser Arg Ser His Ala Thr Trp Ala Arg Cys Ile Val Arg
260 265 270

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CATGGCGGCT CCCTTGGTCC TGGTGCTGGT GGTGGCTGTG ACAGTGCGGG CGGCCTTGTT	60
CCGCTCCAGT CTGGCCGAGT TCATTTCCGA GCGGGTGGAG GTGGTGTCCC CACTGAGCTC	120
TTGGAAGAGA GTGGTTGAAG GCCTTTCACT GTTGGACTTG GGAGTATCTC CGTATTCTGG	180
AGCAGTATTT CATGAACTC CATTAATAAT ATACCTCTTT CATTTCCTAA TTGACTATGC	240
TGAATTGGTG TTTATGATAA CTGATGCACT CACTGCTATT GCCCTGTATT TTGCAATCCA	300
GGACTTCAAT AAAGTTGTGT TTAAAAAGCA GAAACTCCTC CTAGAACTGG AACAGTATGC	360

CCCAGATGTG GCCGAACTCA TCCGGACCCC TATGGAAATG CGTTACATCC CTTTGAAAGT	420
GGCCCTGTTC TATCTCTTAA ATCCTTACAC GATTTTGTCT TGTGTTGCCA AGTCTACCTG	480
TGCCATCAAC AACACCCTCA TTGCTTTCTT CATTTTGA CT ACGATAAAAAG TTTCATTATC	540
TGTAAAATGG GGACAGTAAT TGTACCCACT TCATGGAATT ATTGAGAAGA CTAAATGGCT	600
TAAGGCAGTG CTTTCCTCAG TGCTATTTTT CTTGCCTTAG CGACATACCA GTCTCTGAAC	660
CCACTCACCT TGTTTGTCCC AGGACTCCTC TATCTCCTCC AGCGGCAGTA CATACTGTG	720
AAAAATGAAGA GCAAAGCCTT CTGGATCTTT TCTTGGGAGT ATGCCATGAT GTATGTGGGA	780
AGCCTAGTGG TAATCATTTG CCTCTCCTTC TTCCTTCTCA GCTCTTGGGA TTTCATCCCC	840
GCAGTCTATG GCTTTATACT TTCTGTTCCA GATCTCACTC CAAACATTGG TCTTTTCTGG	900
TACTTCTTGG CAGAGATGTT TGAGCACTTC AGCCTCTTCT TTGTATGTGT GTTTCAGATC	960
AACGTCTTCT TCTACACCAT CCCCTTAGCC ATAAAGCTAA ATCCTGAGAA ACATCTTTGT	1020
CCTCACCTGC ATCATCATCG TCTGTTCCCT GCTCTTCCCT GTCCTGTGGC ACCTCTGGAT	1080
TTATGCAGGA AGTGCCAACT CTAATTTCTT TTATGCCATC ACACTGACCT TCAACGTTGG	1140
GCAGATCCTG CTCATCTCTG ATTACTTCTA TGCCTTCCTG CGGCGGGAGT ACTACCTCAC	1200
ACATGGCCTC TACTTGACCG CCAAGGATGG CACAGAGGCC ATGCTCGTGC TCAAGTAGGC	1260
CTGGCTGGCA CAGGGCTGCA TGGACCTCAG GGGGCTGTGG GGCCAGAAGY TGGGCCAAGC	1320
CCTCCAGCCA GAGTTGCCAG CAGGCGAGTG CTTGGGCAGA AGAGGTTCTGA GTCCAGGGTC	1380
ACAAGTCTCT GGTACCAAAA GGGACCCATG GCTGACTGAC AGCAAGGCCT ATGGGGAAGA	1440
ACTGGGAGYT CCCCAACTTG GACCCCCACC TTGTGGCTCT GCACACCAAG GAGCCCCYTC	1500
CCAGACAGGA AGGAGAAGAG GCAGGTGAGC AGGGCTTGTT AGATTGTGGC TACTTAATAA	1560
ATGTTTTTTT TTATGAAGTC TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA	1613

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ala Ala Pro Leu Val Leu Val Leu Val Val Ala Val Thr Val Arg

1	5	10	15
Ala Ala Leu Phe Arg Ser Ser Leu Ala Glu Phe Ile Ser Glu Arg Val			
20	25	30	
Glu Val Val Ser Pro Leu Ser Ser Trp Lys Arg Val Val Glu Gly Leu			
35	40	45	
Ser Leu Leu Asp Leu Gly Val Ser Pro Tyr Ser Gly Ala Val Phe His			
50	55	60	
Glu Thr Pro Leu Ile Ile Tyr Leu Phe His Phe Leu Ile Asp Tyr Ala			
65	70	75	80
Glu Leu Val Phe Met Ile Thr Asp Ala Leu Thr Ala Ile Ala Leu Tyr			
85	90	95	
Phe Ala Ile Gln Asp Phe Asn Lys Val Val Phe Lys Lys Gln Lys Leu			
100	105	110	
Leu Leu Glu Leu Glu Gln Tyr Ala Pro Asp Val Ala Glu Leu Ile Arg			
115	120	125	
Thr Pro Met Glu Met Arg Tyr Ile Pro Leu Lys Val Ala Leu Phe Tyr			
130	135	140	
Leu Leu Asn Pro Tyr Thr Ile Leu Ser Cys Val Ala Lys Ser Thr Cys			
145	150	155	160
Ala Ile Asn Asn Thr Leu Ile Ala Phe Phe Ile Leu Thr Thr Ile Lys			
165	170	175	
Val Ser Leu Ser Val Lys Trp Gly Gln			
180	185		

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AAACCCTGTC GGTCTTGGAG CGACGACGGC AGAACCAGGG TCCCTGGCGG TGCGGCGGGG	60
CCGGCGGGTG CAGCGGAAGC GGCGGCGGCG GCGGCAGTGA CGTCGCCGGG AACCCTAAGG	120
ACTCTGCAAT ATGAATAATT CCCTAGAGAA CACCATCTCC TTTGAAGAGT ACATCCGAGT	180
AAAGGCACGG TCTGTCCCGC AACACAGGAT GAAGGAATTT CTGGACTCAC TGGCCTCTAA	240

GGGGCCAGAA GCCCTTCAGG AGTTCCAGCA GACAGCCACC ACTACCATGG TGTACCAACA 300
GGGTGGGAAC TGCATATACA CAGACAGCAC TGAAGTGGCT GGGTCTTTGC TTGAACTTGC 360
CTGTCCAATC AC 372

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGGGAAGCTC GAAATGGAGA AGGTGAACCT TATGACCCAG ATGTGCTCTA CTATATTTTC 60
CTGTGTATTC AAAAGTATCT TTTTGAAAAT GGAAGGGTAG ATGACATTTT CTCCGATCTT 120
TATTATGTTT GGTTCACGGA GTGGCTACAT GAAGTTCTGA AGGATGTTCA GCCCCGGGTC 180
ACTCCACTTG GCTATGTCTT GCCCAGCCAC GTGACTGAGG AGATGCTATG GGAGTGCAAG 240
CAGCTTGGGG CTCACTCCCC CTCCACCTTG CTGACCACCC TCATGTTCTT TAATACCAAG 300
TAAGTGTTCCT AGAGGCTCCA CTGCTGGCAT CTGTCCAGTG AAGAGTGTGG AAACATATCCA 360
AGAGGCCTTC TGAATTCCTC TGACATATAT TTGAGAACT GGGCTACTGA AAGCCCTAAC 420
CCCACTTGGC TGCATTTTAT TTGGTAACCA GTGAGGCAAA CACCCTTGCC AGACCCCTAC 480
CATCCATCTT GATGTGGTTC CTGCACTGGA CACTGCTTGG GTACGGGCCT GCCCAGATCT 540
TGGGAATGTG GGCAGTGGCT CCTCTGAAGC ACCAGTGGGC AGAGGATGAG TCATGGTATC 600
CT 602

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Trp Phe Leu His Trp Thr Leu Leu Gly Tyr Gly Pro Ala Gln Ile
1 5 10 15

Leu Gly Met Trp Ala Val Ala Pro Leu Lys His Gln Trp Ala Glu Asp
20 25 30

Glu Ser Trp Tyr Pro
35

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TGGGAAAGGG CTTGGACTGT GAAAAGAAAT GTGGCCCCTT TCCATCTTCA AGAGAGATGG 60
AATTAATGAT GGATGGACCC TGGAGGGAAT CTCCCCAGCC GACTTCCACT GGGCTGACAG 120
ACTTTGCTGA CCACAGGGGA ACGATGTTCT TTTCTTTCTT CATGATCAGA CATAAACTTA 180
GCATTTTAAT GGAAGAAAAA TGAGGGGAAC TTCAATTATG ATTTATTAAA GACAATTTCT 240
ATTACACCCT CCTTTATGAC AAGTGACATT TTAGATGTAA AAGTAAAAAC TTTACCATGC 300
CTTTTTTTTT TTTGTTGGCC TAACATTGAG GCCTTAAAAC CTGAGGCTCC TGTGCCTGAT 360
GGAATTCTTG TAACATACAC TTGTGTATCA TATAAGATA CCACTCTGTT TCTCTTATGT 420
ATTCTTACTC TAGTTGTTTA TTAAGAATGA CAAGCACGTC TTTTCAACAA AAAAAAAAAA 480
AAA 483

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1853 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGATTCGCT GCTGGAGTGC TGGATGGAGC CTTTCTCTGC CCTCTGTGAC ATTTCCAATT 60
 TTAGATAATG CCTCACATCT CTGTCCCCC GGGACCCCT GGAGCCCCCA TGATCCCTAA 120
 GAAGACAGCT TGAACCTAGA TCTACCCCC AGGATGTTGC GGAGGCTGCT GGAGCGGCCT 180
 TGCACGCTGG CCCTGCTTGT GGGCTCCCAG CTGGCTGTCA TGATGTACCT GTCACTGGGG 240
 GGCTTCCGAA GTCTCAGTGC CCTATTTGGC CGAGATCAGG GACCGACATT TGACTATTCT 300
 CACCCTCGTG ATGTCTACAG TAACCTCAGT CACCTGCCTG GGGCCCCAGG GGGTCTCCA 360
 GCTCCTCAAG GTCTGCCCTA CTGTCCAGAA CGATCTCCTC TCTTAGTGGG TCCTGTGTCTG 420
 GTGTCCTTTA GCCCAGTGCC ATCACTGGCA GAGATTGTGG AGCGGAATCC CCGGGTAGAA 480
 CCAGGGGGCC GGTACCGCCC TGCAGGTTGT GAGCCCCGCT CCCGAACAGC CATCATTTGTG 540
 CCTCATCGTG CCCGGGAGCA CCACCTGCGC CTGCTGCTCT ACCACCTGCA CCCCTTCTTG 600
 CAGCGCCAGC AGCTTGCTTA TGGCATCTAT GTCATCCACC AGGCTGGAAA TGGAACATTT 660
 AACAGGGCAA AACTGTTGAA CGTTGGGGTG CGAGAGGCCC TGCCTGATGA AGAGTGGGAC 720
 TGCCTGTTCT TGCACGATGT GGACCTCTTG CCAGAAAATG ACCACAATCT GTATGTGTGT 780
 GACCCCCGGG GACCCCGCCA TGTGCGGTT GCTATGAACA AGTTTGATA CAGCCTCCCG 840
 TACCCCCAGT ACTTCGGAAG AGTCTCAGCA CTTACTCCTG ACCAGTACCT GAAGATGAAT 900
 GGCTTCCCCA ATGAATACTG GGGCTGGGGT GGTGAGGATG ACGACTTGCT ACCAGGGTGC 960
 GCCTGGCTGG GATGAAGATC TCTCGGCCCC CCACATCTGT AGGACACTAT AAGATGGTGA 1020
 AGCACCGAGG AGATAAGGGC AATGAGGAAA ATCCCCACAG ATTTGACCTC CTGGTCCGTA 1080
 CCCAGAATTC CTGGACGCAA GATGGGATGA ACTCACTGAC ATACCAGTTG CTGGCTCGAG 1140
 AGCTGGGGCC TCTTTATACC AACATCACAG CAGACATTGG GACTGACCCT CGGGGTCTCTC 1200
 GGGCTCCTTC TGGGCCACGT TACCCACCTG GTTCTCTCCA AGCCTTCCGT CAAGAGATGC 1260
 TGCAACGCCG GCCCCAGCC AGGCCTGGGC CTCTATCTAC TGCCAACCAC ACAGCCCTCC 1320
 GAGGTTTACA CTGACTCCTC CTTCCTGTCT ACCTTAATCA TGAAACCGAA TTCATGGGGT 1380
 TGTATTCTCC CCACCCTCAG CTCCTCACTG TTCTCAGAAG GATGTGAGGG AACTGAACTC 1440
 TGGTGCCGTG CTAGGGGGTA GGGGCCTCTC CCTCACTGCT GGACTGGAGC TGGGCTCCTG 1500
 TAGACCTGAG GGTCCNTCTY TCTAGGTCTC CTGTAGGGCT TAKGACTGTG AATCCTTGAT 1560
 GTCATGATTT TATGTGACGA TTCTTAGGAG TCCCTGCCCC TAGAGTAGGA GCAGGGYTGG 1620
 ACCCCAAGCC CNTCCYTYTT CCATGGAGAG AAGAGTGATC TGGYTTCTCC TCGGACCTCT 1680
 GTGAATATTT ATTCTATTTA TGGTTCCCGG GAAGTTGTTT GGTGAAGGAA GCCCCCTCCC 1740

TGGGCATTTT CTGCCTATGC TGGGAATAGCT CCCTCTTCTG GTCCTGGCTC AGGGGGCTGG 1800
 GATTTTGATA TATTTTCTAA TAAAGGACTT TGTCTCGCAA AAAAAAAAAA AAA 1853

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met	Leu	Arg	Arg	Leu	Leu	Glu	Arg	Pro	Cys	Thr	Leu	Ala	Leu	Leu	Val
1				5					10					15	
Gly	Ser	Gln	Leu	Ala	Val	Met	Met	Tyr	Leu	Ser	Leu	Gly	Gly	Phe	Arg
			20					25					30		
Ser	Leu	Ser	Ala	Leu	Phe	Gly	Arg	Asp	Gln	Gly	Pro	Thr	Phe	Asp	Tyr
		35					40					45			
Ser	His	Pro	Arg	Asp	Val	Tyr	Ser	Asn	Leu	Ser	His	Leu	Pro	Gly	Ala
	50					55					60				
Pro	Gly	Gly	Pro	Pro	Ala	Pro	Gln	Gly	Leu	Pro	Tyr	Cys	Pro	Glu	Arg
65					70					75				80	
Ser	Pro	Leu	Leu	Val	Gly	Pro	Val	Ser	Val	Ser	Phe	Ser	Pro	Val	Pro
			85					90						95	
Ser	Leu	Ala	Glu	Ile	Val	Glu	Arg	Asn	Pro	Arg	Val	Glu	Pro	Gly	Gly
			100					105					110		
Arg	Tyr	Arg	Pro	Ala	Gly	Cys	Glu	Pro	Arg	Ser	Arg	Thr	Ala	Ile	Ile
			115				120					125			
Val	Pro	His	Arg	Ala	Arg	Glu	His	His	Leu	Arg	Leu	Leu	Leu	Tyr	His
	130					135					140				
Leu	His	Pro	Phe	Leu	Gln	Arg	Gln	Gln	Leu	Ala	Tyr	Gly	Ile	Tyr	Val
145					150					155				160	
Ile	His	Gln	Ala	Gly	Asn	Gly	Thr	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn
			165					170					175		
Val	Gly	Val	Arg	Glu	Ala	Leu	Arg	Asp	Glu	Glu	Trp	Asp	Cys	Leu	Phe
			180					185					190		
Leu	His	Asp	Val	Asp	Leu	Leu	Pro	Glu	Asn	Asp	His	Asn	Leu	Tyr	Val
		195					200					205			

Cys Asp Pro Arg Gly Pro Arg His Val Ala Val Ala Met Asn Lys Phe
 210 215 220

Gly Tyr Ser Leu Pro Tyr Pro Gln Tyr Phe Gly Arg Val Ser Ala Leu
 225 230 235 240

Thr Pro Asp Gln Tyr Leu Lys Met Asn Gly Phe Pro Asn Glu Tyr Trp
 245 250 255

Gly Trp Gly Gly Glu Asp Asp Asp Leu Leu Pro Gly Cys Ala Trp Leu
 260 265 270

Gly

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1686 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGATAAAGTA AGTGCTGTTT GGGCTAACAG GATCTCCTCT TGCAGTCTGC AGCCCAGGAC 60

GCTGATTCCA GCAGCGCCTT ACCGCGCAGC CCGAAGATTC ACTATGGTGA AAATCGCCTT 120

CAATACCCCT ACCGCCGTGC AAAAGGAGGA GCGCGGCAA GACGTGGAGG CCCTCCTGAG 180

CCGCACGGTC AGAACTCAGA TACTGACCGG CAAGGAGCTC CGAGTTGCCA CCCAGGAAAA 240

AGAGGGCTCC TCTGGGAGAT GTATGCTTAC TCTCTTAGGC CTTTCATTCA TCTTGGCAGG 300

ACTTATTGTT GGTGGAGCCT GCATTTACAA GTACTTCATG CCCAAGAGCA CCATTTACCG 360

TGGAGAGATG TKCTTTTTTG ATTCTGAGGA TCCTGCAAAT TCCCTTCGTG GAGGAGAGCC 420

TAACTTCCTG CCTGTGACTG AGGAGGCTGA CATTCGTGAG GATGACAACA TTGCAATCAT 480

TGATGTGCCT GTCCCCAGTT TCTCTGATAG TGACCCTGCA GCAATTATTC ATGACTTTGA 540

AAAGGGAATG ACTGCTTACC TGGACTTGTT GCTGGGGAAC TGCTATCTGA TGCCCCCTCAA 600

TACTTCTATT GTTATGCCTC CAAAAATCT GGTAGAGYTC TTTGGCAAAC TGGCGAGTGG 660

CAGATATCTG CYTCAAACCT ATGTGGTTCG AGAAGACCTA GTTGCTGTGG AGGAAATTCG 720

TGATGTTAGT AACCTTGGCA TCTTTATTTA CCAACTTTGC AATAACAGAA AGTCCTTCCG 780

CCTTCGTCGC AGAGACCTCT TGCTGGGTTT CAACAAACGT GCCATTGATA AATGCTGGAA 840

GATTAGACAC TTCCCCAACG AATTTATTGT TGAGACCAAG ATCTGTCAAG AGTAAGAGGC 900
AACAGATAGA GTGTCCTTGG TAATAAGAAG TCAGAGATTT ACAATATGAC TTTAACATTA 960
AGGTTTATGG GATACTCAAG ATATTTACTC ATGCATTTAC TCTATTGCTT ATGCTTTAAA 1020
AAAAGGAAAA GAAAAAACT ACTAACCCT GCAAGCTCTT GTCAAATTTT AGTTTAATTG 1080
GCATTGCTTG TTTTTTGAAA CTGAAATTAC ATGAGTTTCA TTTTTTCTTT GAATTTATAG 1140
GGTTTAGATT TCTGAAAGCA GCATGAATAT ATCACCTAAC ATCCTGACAA TAAATTCCAT 1200
CCGTTGTTTT TTTTGTGTGT TTGTTTTTTC TTTTCCTTTA AGTAAGCTCT TTATTCATCT 1260
TATGGTGCAG CAATTTTAAA ATTTGAAATA TTTTAAATTG TTTTGAAC TTTTGTGTAA 1320
AATATATCAG ATCTCAACAT TGTGTTTTC TTTTGTTTTT CATTTTGTAC AACTTTCTTG 1380
AATTTAGAAA TTACATCTTT GCAGTTCTGT TAGGTGCTCT GTAATTAACC TGAATTATAT 1440
GTGAACAATT TTCATGAGAC AGTCATTTTT AACTAATGCA GTGATTCTTT CTCACTACTA 1500
TCTGTATTGT GGAATGCACA AAATTGTGTA GGTGCTGAAT GCTGTAAGGA GTTTAGGTTG 1560
TATGAATTCT ACAACCCTAT AATAAATTTT ACTCTATAAA AAAAAAAAAA AAAAAAAAAA 1620
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1680
AAAAAA 1686

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
1 5 10 15
Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln
20 25 30
Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly
35 40 45
Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu
50 55 60

Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
65 70 75 80

Lys Ser Thr Ile Tyr Arg Gly Glu Met Xaa Phe Phe Asp Ser Glu Asp
85 90 95

Pro Ala Asn Ser Leu Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr
100 105 110

Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val
115 120 125

Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp
130 135 140

Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys
145 150 155 160

Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu
165 170 175

Val Glu Xaa Phe Gly Lys Leu Ala Ser Gly Arg Tyr Leu Xaa Gln Thr
180 185 190

Tyr Val Val Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val
195 200 205

Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser
210 215 220

Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
225 230 235 240

Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val
245 250 255

Glu Thr Lys Ile Cys Gln Glu
260

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TNCACATTCTC AGTGGGAACT TGATGAAC

29

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ANATATAGGTG GAATGAATTC TATCCTTG

29

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GNTATAGTAAT AATAGCACAA AGGACGGG

29

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TNGCCAGGAAA CCAAATCAAT GACTCTTT

29

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TNTAATTGACG GTGTAGAGAA ATGAGGAA

29

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ANAAATGGAGC AGCTGGGTGG AGGCAAGA

29

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TNCGGAGATAC TCCCAAGTCC AACAGTGA

29

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GNTTAGGGCTT TCACTAGCCC AGTTTCTC

29

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ANTGACAGGTA CATCATGACA GCCAGCTG

29

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CNGGATGTTAG GTGATATATT CATGCTGC

29

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly	Glu	Val	Lys	Ser	Ser	Gly	Leu	Leu	Cys	Arg	Gly	Thr	Trp	Ala	Trp	1	5	10	15
Ser	Arg	Leu	Pro	Arg	Lys	Cys	Leu	Cys	Val	Gln	Ile	Ser	Arg	His	Leu	20	25	30	
Gly	Lys	Met	Tyr	Ser	Glu	Met	Ile	Phe	Val	Asn	Gly	Phe	Val	His	Cys	35	40	45	
Asp	Pro	His	Pro	Gly	Asn	Val	Leu	Val	Arg	Lys	His	Pro	Gly	Thr	Gly	50	55	60	
Lys	Ala	Glu	Ile	Val	Leu	Leu	Asp	His	Gly	Leu	Tyr	Gln	Met	Leu	Thr	65	70	75	80
Glu	Glu	Phe	Arg	Leu	Asn	Tyr	Cys	His	Leu	Trp	Gln	Ser	Leu	Ile	Trp	85	90	95	
Thr	Asp	Arg	Lys	Arg	Val	Lys	Glu	Tyr	Ser	Gln	Arg	Leu	Gly	Ala	Gly	100	105	110	
Asp	Leu	Tyr	Pro	Leu	Phe	Ala	Cys	Met	Leu	Thr	Ala	Arg	Ser	Trp	Asp	115	120	125	
Ser	Val	Asn	Arg	Gly	Ile	Ser	Gln	Ala	Pro	Val	Thr	Ala	Thr	Glu	Asp	130	135	140	
Leu	Glu	Ile	Arg	Asn	Asn	Ala	Ala	Asn	Tyr	Leu	Pro	Gln	Ile	Ser	His	145	150	155	160
Leu	Leu	Asn	His	Val	Pro	Arg	Gln	Met	Leu	Leu	Ile	Leu	Lys	Thr	Asn	165	170	175	
Asp	Leu	Leu	Arg	Gly	Ile	Glu	Ala	Ala	Leu	Gly	Thr	Arg	Ala	Ser	Ala	180	185	190	
Ser	Ser	Phe	Leu	Asn	Met	Ser	Arg	Cys	Cys	Ile	Arg	Ala	Leu	Ala	Glu	195	200	205	
His	Lys	Lys	Lys	Asn	Thr	Cys	Ser	Phe	Phe	Arg	Arg	Thr	Gln	Ile	Ser	210	215	220	
Phe	Ser	Glu	Ala	Phe	Asn	Leu	Trp	Gln	Ile	Asn	Leu	His	Glu	Leu	Ile	225	230	235	240
Leu	Arg	Val	Lys	Gly	Leu	Lys	Leu	Ala	Asp	Arg	Val	Leu	Ala	Leu	Ile	245	250	255	
Cys	Trp	Leu	Phe	Pro	Ala	Pro	Leu	260											

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CGCTTTTTTT TTTTTTTTTT TTCAGAAGGA GGAAGCTCAT TATGTTTGA TCACCCACAG	60
CTATAGATTC TAAAAATATT TTGGCTTTTT TTGAGGTGCT TTAGTAAAAT ATAACCCCAA	120
ATGATTCACT TGGACAAGTG GTCTTAACAG CAAGGAAAAC AAACACTTTA TGAAAACAGC	180
TATAAGCCTT CTGTCTTTTA TCTTTACTAT TTTCTCCGAG TCTGGCATGA AACAGATACA	240
CAGCAGCCTC CACAGGGGGT TAAGTARAGA ACCATCCAAG CATCACAGAG TGTCATCCAG	300
AATTCTGATG ACTTCCATTC GTTGACTCTG ATGCACAATA TGCCTGGCTT GGGATGCAGC	360
GACCATGATG CCCCTCCCAG AACAGACACT TGCAGAGTGT TCCAGGAACA GCAGCTCCCT	420
CCAGCCCCCA GCACAAGATG CACACATCTC AGAACAAGCC TCCATCCTTT TCCTAGAGAA	480
CTGAGCATAA ATAACTTGTT CTATATCTGG CTCCAAGTCC ATTTCTGTTC TGTCTTGAG	540
TAGAGTCTTA GCTCCCAGTT TGTTTTAGGT CAACTTTCAG CACCTACTTC AGCTCACTTG	600
TTTGATTTAC TAAGCTCTTG CTTCTGTATA TTATCAAATG TAGGGATGTA GGGAGAATAA	660
AAGGATCTAG AACTTGCTT TTAGGAGAGA TTAGAACAAA GCTGAAGGTG GAGGCATTAG	720
TTCTAGGTC TTCAGATCTC AGAGCAAAGG ACCCACTCTG GAGCCTAAAT TCTATGAGAG	780
ACCACAGAGC AGCCTGAAAT CCAAAGGAGT TTTACACAGG AAAAAAAAAA TACTGTGAGG	840
ACTTACACTA AATAATAATG TTGTTTGA TGGGGTTGTG GGTAATTCCT ATATTCTTCT	900
TTATAACTTT TGTACTTTTC AAATCCCTA ATGTGAACTC ACTACTTAGT AGGTCTGTAA	960
GCTTAAACAT TACTATGGCT TGGAATCTCA TTTCAAAAAA TCTTTAAAAT GGGGACAAGA	1020
GTAAAAATTT CTTAGCTTCT ATGGAAGAAT AAAATGAAAT TATAATGATA CAGTGCCTGG	1080
CATGTTGTGG TCGCTCAATA AACACTGCTT TCCTCCCCAT TGTCTCTCTC TTTATTCTGT	1140
TTCATTACAA GGTCAGCAGA TTGAATCAGG ACCAGCTGGG AGGGCTACTT CTATGAGAGA	1200
AGATCTGTCC ACAGTCATGG TTTTCAATGT TTAGTGCACC AGAATCACCT TGAGGGTTTG	1260
TTAAAACAGA CTGCTGAACA TAACACATCT ATGAGAATGG CCAAAATCCA GAACACCAAA	1320
TGCTGGTGAG GATGTGGAGC AATAAAAACT CTCATTTATT GCTGATGGCA ATGCAAAATG	1380

GTACAGCCAC TTTGGAAGAC AATTTGCCAA ATTTTACAA AACTAAGTGT ACTCTTACCA 1440
TACAATCTAG CAATCATGCT CCCTGGTATT TACCTAAAGG AGTTAAAAAC TTATGTCTAG 1500
ACAGAAACCT GCATATGAAT GTTTATAGCA GTTTTTTTCA TAATTGCTAA ACTTTGGAAG 1560
TAACCAAGAT GCCCTTCAGC AGGTGAATGG ACAAATAAAC TGCAGTAGAT GCAGACAGTG 1620
GAATATCATT CTAGGCCATG AAGGCCGAAT TCGGCCTTCA TGGCCTAATT AAAGAAAGTC 1680
AGGATAAAAA TTTTAAAAAG CAGGCCACTG TCAGCAAAGC CTGGAGAAGT GGGGCCGGAG 1740
GYTCCGCCCC CATCATGTGC CTGCCACCCC TTCCCAGTCA TCCCTTTAYT CTTACAGTAG 1800
CAAATAAGAC CCCTGTCTAA TGGGGGGAGA CAAATGTGTA GACCCTTAGC CACCTTGGCC 1860
AGGGCTGACT CCTTAAATTT CTGGATGATG ATGATTGTTA TTTAATAGCC AGAGGCTCAT 1920
ATAATTGGCC TCTTTGGAAG AGGCCTCATG GCCTCCTTAC TCTCACCAA GCAATTTTTC 1980
CCTCAGGGGG GCTCCCATCT TCTTACACAG AGAGGCAGCT GAGGCAGGAC AGTGGGGCTA 2040
ACTGTAGACC AGGCGAGGGC ACGGGCTGCT GGGGTGGCCC TGCTTCCCCA GTGTACATAT 2100
TGTATCTGTG TAACATTTTG TATATTCCAG GGGTAGGGCC GCCCCCTGTA TCATACCTAG 2160
CAGAGGTTGG AGCTGGCACA TGGGGAGGAG GTTCTAATAA TTATTTGGGG CTGGGAAACT 2220
TATTTATTGA TAGCATAGGA CAGAGGAAGG AGGCGGGGAT GGGGTCGTGG CGCCCTGGTG 2280
ATGCGACTCC TGTTTATTTT GCTTTTATT TCGGAATAAA TGGATTTAGC CATAAAAAAA 2340
AAAAAAAAAA AAAAA 2355

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met	Lys	Thr	Ala	Ile	Ser	Leu	Leu	Ser	Phe	Ile	Phe	Thr	Ile	Phe	Ser
1				5					10					15	
Glu	Ser	Gly	Met	Lys	Gln	Ile	His	Ser	Ser	Leu	His	Arg	Gly	Leu	Ser
			20					25					30		
Xaa	Glu	Pro	Ser	Lys	His	His	Arg	Val	Ser	Ser	Arg	Ile	Leu	Met	Thr
			35				40						45		

Ser Ile Arg
50

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GCGCCCTTTC GGTCAACATC GTAGTCCACC CCCTCCCCAT CCCAGCCCC CGGGGATTCA	60
GGCTCGCCAG CGCCAGCCA GGGAGCCGGC CGGGAAGCGC GATGGGGGCC CCAGCCGCCT	120
CGCTCCTGCT CCTGCTCCTG CTGTTGCGCT GCTGCTGGGC GCCCGCGGG GCCAACCTCT	180
CCCAGGACGA CAGCCAGCCC TGGACATCTG ATGAAACAGT GGTGGCTGGT GGCACCGTGG	240
TGCTCAAGTG CCAAGTGAAA GATCACGAGG ACTCATCCCT GCAATGGTCT AACCTGCTC	300
AGCAGACTCT CTACTTTGGG GAGAAGAGAG CCCTTCGAGA TAATCGAATT CAGCTGGTTA	360
CCTCTACGCC CCACGAGCTC AGCATCAGCA TCAGCAATGT GGCCCTGGCA GACGAGGGCG	420
AGTACACCTG CTCAATCTTC ACTATGCCTG TCGGAACTGC CAAGTCCCTC GTCACTGTGC	480
TAGGAATTCC ACAGAAGCCC ATCATCACTG GTTATAAATC TTCATTACGG GAAAAAGACA	540
CAGCCACCCT AAAGTGTCTG TCTTCTGGGA GCAAGCCTGC AGCCCGGCTC ACCTGGAGAA	600
AGGGTGACCA AGAACTCCAC GGAGAACCAA CCCGCATACA GGAAGATCCC AATGGTAAAA	660
CCTTCACTGT CAGCAGCTCG GTGACATTCC AGGTTACCCG GGAGGATGAT GGGGCGAGCA	720
TCGTGTGCTC TGTGAACCAT GAATCTCTAA AGGGAGCTGA CAGATCCACC TCTCAACGCA	780
TTGAAGTTTT ATACACACCA ACTGCGATGA TTAGGCCAGA CCCTCCCCAT CCTCGTGAGG	840
GCCAGAAGCT GTTGCTACAC TGTGAGGGTC GCGGCAATCC AGTCCCCCAG CAGTACCTAT	900
GGGAGAAGGA GGGCAGTGTG CCACCCCTGA AGATGACCCA GGAGAGTGCC CTGATCTTCC	960
CTTTCCTCAA CAAGAGTGAC AGTGGCACCT ACGGCTGCAC AGCCACCAGC AACATGGGCA	1020
GCTACAAGGC CTACTACACC CTCAATGTGA ATGACCCAG TCCGGTGCCC TCCTCCTCCA	1080
GCACCTACCA CGCCATCATC GGTGGGATCG TGGCTTTCAT TGTCTTCCTG CTGCTCATCA	1140
TGCTCATCTT CCTCGGCCAC TACTTGATCC GGCACAAAGG AACCTACCTG ACACATGAGG	1200
CAAAAGGCTC CGACGATGCT CCAGACGCGG ACACGGCCAT CATCAATGCA GAAGGCGGGC	1260

AGTCAGGAGG GGACGACAAG AAGGAATATT TCATCTAGAG GCGCCTGCCC ACTTCCTGCG 1320
 CCCCCAGGG GCCCTGTGGG GACTGCTGGG GCCGTCACCA ACCCGGACTT GTACAGAGCA 1380
 ACCGCAGGGC CGCCCCTCCC GCTTGCTCCC CAGCCCACCC ACCCCCCTGT ACAGAATGTC 1440
 TGCTTTGGGT GCGGTTTTGT ACTCGGTTTG GAATGGGGAG GGAGGAGGGC GGGGGGAGGG 1500
 GAGGGTTGCC CTCAGCCCTT TCCGTGGCTT CTCTGCATTT GGGTTATTAT TATTTTTGTA 1560
 ACAATCCCAA ATCAAATCTG TCTCCAGGCT GGAGAGGCAG GAGCCCTGGG GTGAGAAAAG 1620
 CAAAAACAA AAAAAAACA AAACCCTGGA GTGTTAGGAG GAGAGTGAAG GTAGAGGGGT 1680
 GAGGAAGGGT AAGGGGCAGG GCTGGTTTCA GCTGGGGGCT CTCACCAGCC CTCCTTTCAG 1740
 CCTCTACAAC AGAGCAGCTT CCCAGACTTC TCCAGGAACC CAGAAACGGG ATGGTTGTCTG 1800
 GCAAAGGTTG GGAGTGGCTT TTCCTCTGGT AGCCACACAC CTGAGCACTA CGGACAGGGA 1860
 GGCAGGTGCC ACCTTGACAC CTCTCTTCCA TAGCAATGGG AAAGTGATGA GTGCGGGAGT 1920
 CCTGAGGAGA TGTGGCCTGC AGACAACATG CAGCCATGCA GGGACCCAGG ACTGTAACCT 1980
 GGGGAGGACG CGGGTCCCTG CAAGGAAGAG TAGATTTGGA GAGGAAGGAT GGAGGTGGAC 2040
 TCTCACCCCA TTCCCCCGG AAATGAACAA AGCCGGGCCC TTTCCATAGG AACTGCCCTT 2100
 GGAGATAGCA GAGTGTGGCT GCCCCTCCTT GCTCCAGCAG CAGTGGGAGA GGCAGTCTC 2160
 TGGGGCCTGA ACTGCCTCTG CTTCCCCCCC TGAGGGGCCC CTCACTCTTA CCAAGACTC 2220
 TGGATTGTTG CACGGCAACC ACTCCTCCCA TGGCATTGCT CAGCAACTAC TTCTCCCTTC 2280
 CCGGCCACCC TGTGCCCCCT TCCTGGTCCC AACGCCAGCC CTTCATCCTT CCTCCCTCAG 2340
 CAGCCAGGCA GACATAACAA CAAAACACT AAAAGGAGCT TCAAAAAAA AAAAAAAAAA 2400
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 2496

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala

1		5						10					15			
Cys	Cys	Trp	Ala	Pro	Gly	Gly	Ala	Asn	Leu	Ser	Gln	Asp	Asp	Ser	Gln	
			20					25					30			
Pro	Trp	Thr	Ser	Asp	Glu	Thr	Val	Val	Ala	Gly	Gly	Thr	Val	Val	Leu	
		35					40					45				
Lys	Cys	Gln	Val	Lys	Asp	His	Glu	Asp	Ser	Ser	Leu	Gln	Trp	Ser	Asn	
	50					55					60					
Pro	Ala	Gln	Gln	Thr	Leu	Tyr	Phe	Gly	Glu	Lys	Arg	Ala	Leu	Arg	Asp	
65					70					75					80	
Asn	Arg	Ile	Gln	Leu	Val	Thr	Ser	Thr	Pro	His	Glu	Leu	Ser	Ile	Ser	
				85					90					95		
Ile	Ser	Asn	Val	Ala	Leu	Ala	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Ser	Ile	
			100					105					110			
Phe	Thr	Met	Pro	Val	Arg	Thr	Ala	Lys	Ser	Leu	Val	Thr	Val	Leu	Gly	
		115					120					125				
Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu	
	130					135						140				
Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala	
145					150					155					160	
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro	
				165					170					175		
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser	
			180					185					190			
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val	
		195					200					205				
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser	
	210					215					220					
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp	
225					230					235					240	
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly	
				245					250					255		
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser	
			260					265					270			
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe	
		275					280					285				
Leu	Asn	Lys	Ser	Asp	Ser	Gly	Thr	Tyr	Gly	Cys	Thr	Ala	Thr	Ser	Asn	
	290					295					300					
Met	Gly	Ser	Tyr	Lys	Ala	Tyr	Tyr	Thr	Leu	Asn	Val	Asn	Asp	Pro	Ser	

305		310		315		320
Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile						
		325		330		335
Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly						
		340		345		350
His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys						
		355		360		365
Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu						
		370		375		380
Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile						
		385		390		395

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2764 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGCCAAAGA GGCCTACCAG CTGCTGTTGA CCGCTGGACT CACAAACCTT TCTTTCTACT	60
CTTGTTTTTC ATTCACTTTG GGTCATTTTT CAGTGTGTGAT GGGGACGTAA TAAAGCACGG	120
TAAGAAAATC CGTGAATTCC GTCAGAGCAG TCGTCCAGAG GGAAGGCGCG CCCGGCGTAG	180
GGAGGTCAGA GCTCATGTTA GCTATGAACA CAGGTCACAG GGGCGTACGG CGATGGGAAA	240
CACTGAGATG CTCAATATAT TGATTATTTA ATAGTGTTTA GCAAAATGGT CTTTTTTTAT	300
TCCTTAAATC AACTGAAACT CACTTCACGT CTCTTTCCTT GTAGAGCATC ATGCTTATTT	360
CTGGCTCACT CACATCTTTG TCTCGGGAGT TCTCTGCCGA GCCATTGCCC CCTACAGCAG	420
AGAGCACAGC TGGCTGCACT AGTGCTGAAG GAGCCAGCCC CAGAGCAGGG CATTTCCAGG	480
GGCTCTTGTC CCAGAGCGGC AGGCGTTGTG TGCAGAGAAC GCCCCTCCCA CGCAGCACAG	540
AGAACGCGGG GTGGGTGTGT GGCTCCGGGC CTGTGGGGCT TAGGCTGCCT GAACCACCGC	600
CGACTGGCAC CATGACTCGG CATTCCTGGA AGTGCCTTAC CAAGTTGTTG TTGTTGTTTT	660
GTTGTTTTTT AAGAGACGGG CTTGCTCTAT CATCCAGGCT CGAGTGCAAT GGCACAGTCA	720
CAGCTCACTG CAGCCTTGAA CTCGTGGGCT CAAGCCATCC TCCTGTGTCA GCCTCCCCAG	780

TACCTGGGAC	TGTGGGCATG	AGCACTGCGC	CTGGCAGCTG	TATCAGTGTT	GACTCCACAT	840
TTTAATAGTT	GCTTCTTGAA	ATTAAAAATGC	TTTGATTGAG	CCTTCAAGCC	ATCAGGAAAG	900
TTTGCCCTC	TGAGTCACAC	CTGGTGGTCT	CCAGGGTTCC	TGCCCCCTCC	TCCTGAGCCA	960
GCTCCTCAGA	GCGGATAGAG	GCAGGACCCC	CACCCAGGTC	TTGAGACCCC	CCTGCCCCGC	1020
ACTCCCCCGG	AGACGGGCTA	CCCCTGCAGA	TGCAGATAGT	CAAAGCTCAG	GTTTCTTCCA	1080
AAGCTTTTAA	AAAGATATTG	TACCTTGAGC	ACTTTAAAAA	TGTCTTAAAA	TTGCCATACA	1140
GGCTCTTAAA	AGCTTATACG	TTTAAACTGT	TGATAGATGG	GCCTTTACTA	AAATGCATTC	1200
ATTTATTTTC	CTAATCCCTT	GGTTGTTAAA	TAATTCTGGG	GAAGGGCCCC	GAGCACGACA	1260
GCCGCAGTCT	CCACCCAGAA	CCAGAGAGTC	CCCCCAACC	CGGGATGTAC	CCTCTGGCCA	1320
CACCAGGGAC	CCTGCCAGAG	GCCGCAGACT	GGCAGCAGCA	GCCTCCCCAC	ACAGTGGGGG	1380
AAGGTCAGTG	TGATGCCTTC	AGGCCCCGTC	TCCTGCCAGG	GCTCTCCCTC	CAGCCTACAT	1440
AGGGCCTCAG	AGAAATGCAT	TTTTAGTTCT	GGCTTTGGCC	CAGCCCAGGG	CAAGGCAGGA	1500
AACTCTCCAG	CGTGAGTCCG	TGAGGGCCAA	GAAGTCCCGC	CCTGTTCTGG	GGGAGGACCT	1560
GGCTTTTCTG	GTGTCTCTGG	TGCCCCGAGAG	CCCGGTGCTG	CCATCTTTAG	TGAAAGAGTA	1620
AATGGTGGCC	GAGGGCTCCT	TTTGTGAGGG	ATGTGCCTTG	GTGAAGAAGG	CATGTTCCCT	1680
GCCGTGAAGA	TACTTGGAAG	CTCTGGGTGG	AGAGGGAAAA	GGGATACCCC	TGGTGCTCCC	1740
TGGGCCTGGC	GGAAGGCTAG	GAGGAAGGAC	AGCTGAGGTG	AGGACTGAGT	GGGGCAGGTA	1800
TCACCCTGAC	AAACAGTTTG	GGAAGATCAG	GAAAGGCAGG	TGAGACCTGG	TGCAGAATCC	1860
AGGTTGGGTA	ATAGATACAT	CGTCGAAGAT	GTAGCAAGCA	AAGTAATATA	CTCAACTCTG	1920
GAACATTGCA	CAGAAGCTTT	TAAAGCACTC	TGTGACACTT	TTTGTAATGA	GGGATCTGAA	1980
GGAAACGGCC	CCAGAGTCAC	CCATCCCCAC	GGGTCTGGTT	GGCGGGGCTG	GTGCCTTTCT	2040
TCTGCACTCA	GTCACCATGG	CTCCGTCTGT	CAAACCAAC	TCTTTTTTTT	TTTTTTTTTC	2100
TTCTCTTGGT	GTGGTAATTT	GTTTGAAGAG	CCACTCCATC	CCCAAATTCA	AGATTAGAAA	2160
GATCCCTGAC	TGCTTCTCAA	GATCCAGAAC	ATTCCTTGAC	AGAGTATATT	CACCATTTAG	2220
AAGTGATCCA	GCAAAGATTG	GGAGGGGTAC	TACCAGATTC	TACTTCAAAG	AAATCCTGCC	2280
ACCCGATGAT	TAAACAGTGA	ATAAAATGTC	ATGGCTCTTT	CCTGCGACAA	TTCTATTTGA	2340
GGAAAAGATT	TGTTTTTCCC	TTTTCCCAAG	GAAGCTCGTG	GGACAGCATG	GGCACTACTC	2400
TTCATGTGCG	GTGACACCAG	CCCCCAGATG	CCTTGAATTA	AGTGTCTCA	CCTTTATGCA	2460
TGACTGCAAA	GCCAGCTGGA	GCATTTTCTA	TGGAGCCTCC	GTATGTTTTA	GGCCCATGAC	2520

CTTCGTGAGG TGATGGGCAC TCACTCCCAT GAGCCCTGGC TGTGTGCTGT TGTGTGCCTA 2580
 TCGGCAGATC CATCCTTCCT GCCTCCAAGG AGGATACACA GAGAATGGCT TCCTGTTGTT 2640
 TTGTTTATTT TCTTAACGTG TACAGATGGA AACTTCATTT AAAAATAAAA ACAAACAAY 2700
 TCNAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760
 AAAA 2764

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Leu Ile Ser Gly Ser Leu Thr Ser Leu Ser Arg Glu Phe Ser Ala
 1 5 10 15
 Glu Pro Leu Pro Pro Thr Ala Glu Ser Thr Ala Gly Cys Thr Ser Ala
 20 25 30
 Glu Gly Ala Ser Pro Arg Ala Gly His Phe Gln Gly Leu Leu Ser Gln
 35 40 45
 Ser Gly Arg Arg Cys Val Gln Arg Thr Pro Leu Pro Arg Ser Thr Glu
 50 55 60
 Asn Ala Gly Trp Val Cys Gly Ser Gly Pro Val Gly Leu Arg Leu Pro
 65 70 75 80
 Glu Pro Pro Pro Thr Gly Thr Met Thr Arg His Ser Trp Lys Cys Leu
 85 90 95
 Thr Lys Leu Leu Leu Leu Phe Cys Cys Phe Leu Arg Asp Gly Leu Ala
 100 105 110
 Leu Ser Ser Arg Leu Glu Cys Asn Gly Thr Val Thr Ala His Cys Ser
 115 120 125
 Leu Glu Leu Val Gly Ser Ser His Pro Pro Val Ser Ala Ser Pro Val
 130 135 140
 Pro Gly Thr Val Gly Met Ser Thr Ala Pro Gly Ser Cys Ile Ser Val
 145 150 155 160
 Asp Ser Thr Phe

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CAGAAGGGAG GTAGTCGCCC TCCGTCGTGG CCTGGCGTGG ATTCCGAGCG TTGGTGTCTG	60
GCGGTTTCCG ACCGTTGGTG TCTGGCACGC GCCACCCCGA TGTACCAGGT AAAGCCCTAT	120
CACGGGGTCG GCGCCCCTCT CCGTGTGGAG CCCACCTGCA TGTACTGGCT CCCCACATG	180
CACGGCAGGA GCGGCGGCCC AGCACTCGGC ACTGGCCACT TGCAGACAAG AAGACAAGAA	240
AATGATTTGA GGACAGCTTC AATCGCGGTG TGAAGAAGAA AGCAACAAAA CGACCACTGA	300
AAACAATGCC GGTGGCAAAA CATCCAAAGA AAGGGTCCCA AGCGGTACAT CGTCATAGCT	360
GGAAACAGTC AGAGCCACCA GCCAATGATC TTTTCAATGC TGCAGAAAGCT GCCAAAAGTG	420
ACATGCAGTG TGGCCATGAG GTCTGCCGGA AGTGA CTGTGTATC TCCTGAGTTA	480
AAATGTGAAG GGATTTTTTT TTTTCAGATT ACTGAGAGTC TTCTGT TACT AGTTTGTCTT	540
TCCTAGATCC AGACACGGGG ACTGCAGAGA AAGGCTGTGT GCATCCGCTG TCTACTCCAC	600
TGTCTCCTCT GCAGAGGCGG ATTTCCCTGA CTGAAGACCA TGTTCAGGC CCACAGCTGC	660
CTACAGAACC GTCCCAAAAT ATGGCAAAGA AACCTATTCT GAGGGTCTCA CCATGTTGCC	720
CAGGCTGGTC TTGAACTCCT GGA CTCTCATCC TAAAGTGCTG GCCTCTCATT CCCTGTCTGT	780
GCACACCTCA CGGCAAGGGC CAGCCTGTTT CCTCCCGGTC ACCTCCAAAT CTTGCTGCTT	840
TTAATTCAAC TCAGAGGCCT AGCCAGGGTT GAGTTCTCAC CCACCTGTGC CGCCCTGCCT	900
TGTTACCTGG AAGCACAGCC TTGGGGACTG AGCAGGCCCT CACTGTCACT TTAAGAAGGG	960
AATCAGCCAC TTTGTGCTCA CCACCTCTGG GGAAGGTGTG AGAGGAGAGA AGGAAGTGGC	1020
TGTTTGGCTG CTGACAACAT GAAGACTTCC TGCATGAGA ACAGAGGCAC AGGTGCCGGC	1080
CCTGCAGCCC CCAGAACCCG GACTGGAGGG GGCCATGGGG CGCCGGACCC TGGCCCTGCC	1140
CTGGGTGCTG CTGACCCTGC GTGTCACTGC AGGGACCCCG GAGGTGTGAG TACAAGTTCTG	1200
GATGGAGGCC ACCGAGCTCT CGTCCTTCAC CATCCGTTGT GGGTTCCTGG AGTCTGGCTC	1260
CATCTCCCTG GTGACTGTGA GCTGGGGGGG CCCCATGGT GCTGGGGGGA CCACGCTGGC	1320

TGTGTTGCAC	CCGGAAC TTG	GCATCCAGCA	ATGGGCCCCCT	GCTCGCCAGG	CCCGCTGGGA	1380
AACCCAGAGC	AGCGTCTCTC	TTGCCCTGGA	AGTCTCTGGG	GCCAGCAGCC	CCTGCACCAA	1440
CACCACCTTC	TGCTGCAAGT	TTGCGTCCTT	CCCTGAGGGC	TCCTGGGAGG	CCTCTGGGAG	1500
CCTCCCGCCC	AGCTCAGACC	CAGGGCTCTC	TGTCCCGCCG	ACTCCTGCCC	CCATTCTGCG	1560
GGCAGACCTG	GCCGGGATCT	TGGGGGTCTC	AGGAGTCCTT	CTCTTTGACT	GTGGCTACCT	1620
CCTTCATCTG	CTGTGCCGAC	AGAAGCACCG	CCCTGCCCCCT	AGGCTCCAGC	CATCCCACAC	1680
CAGCTCCTAG	GCACTGAGAG	CACGAGCATG	GGCACCCAGC	CAGGCCTCCC	AGGCTGCTCT	1740
CCACGTCCCT	TATGCCACTA	TCAACACCAG	CTGCTGCCCA	GCTACTTTGG	ACACAGCTCA	1800
CCCCCGACAG	GGGGCCGTCC	TGTCGTTTCC	TGCTGTGACT	AAGTCAGCAA	CACAGTTCCT	1860
CTGACATGGG	CCTTGGCTGT	GCTTCTTTGG	GGGTGAAGAG	ATTGGGGAGG	AAGTCTCCAC	1920
CCCTGGGAGG	CAGAAGCCAG	GCATAGCGCG	CTGGCTAGGA	CTCCAGTACC	GTGAAGGGAG	1980
GCAGTGAGAG	CAGACATCTG	TGTCTCATTC	CTGATCTCAA	GGGGAAAGCA	AGAACAAGGG	2040
AGGCTTCCTC	AGGATCTCAA	ACCTGCGGAA	GGAGGACCAG	TCTGTGTACT	TCTGCCAAGT	2100
CCAGCTGGAC	ATACAGATCA	GCCCTCAGGC	AGCCCCCTCA	CAGGACCCCT	CTCCTGCCTG	2160
GACAGCTCTG	CTGGTCTCCC	CGTCCCCTGG	AGAAGAACAA	GGCCATGGGT	CGGCCCCCTG	2220
TGCTGCCCCCT	GCTGCTCCTG	CTGCAGCCGC	CAGCATTTCT	GCAGCCTGGT	GGCTCCACAG	2280
GATCTGGTCC	AAGCTACCTT	TATGGGGTCA	CTCAACCAAA	ACACCTCTCA	GCCTCCATGG	2340
GTGGCTCTGT	GGAAATCCCC	TTCTCCTTCT	ATTACCCCTG	GGAGTTAGCC	ACAGCTCCCG	2400
ACGTGAGAAT	ATCCTGGAGA	CGGGGCCACT	TCCACGGGCA	GTCCTTCTAC	AGCACAAGGC	2460
CGCCTTCCAT	TCACAAGGAT	TATGTGAACC	GGCTCTTTCT	GAAGTGGACA	GAGGGTCAGG	2520
AGAGCGGCTT	CCTCAGGATC	TCAAACCTGC	GGAAGGAGGA	CCAGTCTGTG	TATTTCTGCC	2580
GAGTCGAGCT	GGACACCCGG	AGATCAGGGA	GGCAGCAGTT	GCAGTCCATC	AAGGGGACCA	2640
AACTCACCAT	CACCCAGGCT	GTCACAACCA	CCACCACCTG	GACGCCCAGC	AGCACAACCA	2700
CCATAGCCGG	CCTCAGGGTC	ACAGAAAGCA	AAGGGCACTC	AGAATCATGG	CACCTAAGTC	2760
TGGACACTGC	CATCAGGGTT	GCATTGGCTG	TCGCTGTGCT	CAAAACTGTC	ATTTTGGGAC	2820
TGCTGTGCCT	CCTCCTGTGG	TGGAGGAGAA	GGAAAGGTAG	CAGGGCGCCA	AGCAGTGACT	2880
TCTGACCAAC	AGAGTGTGGG	GAGAAGGGAT	GTGTATTAGC	CCCGGAGGAC	GTGATGTGAG	2940
ACCCGCTTGT	GAGTCCTCCA	CACTCGTTCC	CCATTGGCAA	GATACATGGA	GAGCACCTG	3000

AGGACCTTTA AAAGGCAAAG CCGCAAGGCA GAAGGAGGCT GGGTCCCTGA ATCACCGACT 3060
GGAGGAGAGT TACCTACAAG AGCCTTCATC CAGGAGCATC CACACTGCAA TGATATAGGA 3120
WTGAGGTCTG AACTCCACTG AATTAAACCA CTGGCATTG GGGGCTGTTC ATTATAGCAG 3180
TGCAAAGAGT TCCTTTATCC TCCCCAAGGA TGGAAAATAC AATTTATTTT GCTTACCATA 3240
CACCCCTTTT CTCTTCGTCC ACATTTTCCA ATCTGTATGG TGGCTGTCTT CTATGGCAGA 3300
AGGTTTGGG GAATAAATAG CGTGAAATGC TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3360
AAAAAAA 3367

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met	Gly	Arg	Pro	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Gln	Pro	Pro	1	5	10	15		
Ala	Phe	Leu	Gln	Pro	Gly	Gly	Ser	Thr	Gly	Ser	Gly	Pro	Ser	Tyr	Leu	20	25	30	
Tyr	Gly	Val	Thr	Gln	Pro	Lys	His	Leu	Ser	Ala	Ser	Met	Gly	Gly	Ser	35	40	45	
Val	Glu	Ile	Pro	Phe	Ser	Phe	Tyr	Tyr	Pro	Trp	Glu	Leu	Ala	Thr	Ala	50	55	60	
Pro	Asp	Val	Arg	Ile	Ser	Trp	Arg	Arg	Gly	His	Phe	His	Gly	Gln	Ser	65	70	75	80
Phe	Tyr	Ser	Thr	Arg	Pro	Pro	Ser	Ile	His	Lys	Asp	Tyr	Val	Asn	Arg	85	90	95	
Leu	Phe	Leu	Asn	Trp	Thr	Glu	Gly	Gln	Glu	Ser	Gly	Phe	Leu	Arg	Ile	100	105	110	
Ser	Asn	Leu	Arg	Lys	Glu	Asp	Gln	Ser	Val	Tyr	Phe	Cys	Arg	Val	Glu	115	120	125	
Leu	Asp	Thr	Arg	Arg	Ser	Gly	Arg	Gln	Gln	Leu	Gln	Ser	Ile	Lys	Gly	130	135	140	
Thr	Lys	Leu	Thr	Ile	Thr	Gln	Ala	Val	Thr	Thr	Thr	Thr	Thr	Trp	Thr	145	150	155	160

Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys
165 170 175

Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
180 185 190

Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
195 200 205

Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser Ser
210 215 220

Asp Phe
225

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3899 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGGAAGAGAT GGTGACTGAG GCAGAAGCTA ATAGGGAAGA TGATAGGAAA GAAATTTTAC	60
CCAAGGGAAT TAGATTTAGC AAGAGAGCGA AGGAAAGCTG AGAGGCCAAA AACATCTCTG	120
AGGAAACTG ACTCTGAGAG AGAAGAGGTG ACAAGGGCAA ATGCACTCAA GGATGAAGAT	180
GCTTTTAAAG AAGAGCAAAA ACTTAAAGCG GAAGAAGGGG AAACAGAGAC AGAAGTWAGA	240
GCTGAGGAAG AGACAAAAGC TCCCCCAAAT GAAATGGGAT CTGATGCTGA RAACGAASCA	300
CCTGTGGAGG CTTCTGAGTT GTCTGACAAT CCAGGGCTTC TAGGAGAARA TTCACTAAAA	360
GAGACAGTGG TTCCCATATT TGAAGCAACG CCTGGATTTC AAAAGTCGCT GGAAAACATA	420
ACAGCTCTGA GGAAAGAAGG AGGAGGGGAA AGACTGAGTG AAGCCAGAGA CACAGAGCAC	480
AAAGACAGAG AAGAGCTGTC CAGCAGGGAG AATAGGGCCC TGAAGGAAGG GCACCGCCAA	540
GATGGAGAGG GGGCCTTAGC AGCTCCTGAA GCTGAGCCAG CAGGAAAGGT GCAGGCCCTT	600
GAGGGGCTGA TCCCAGCCAC AGGCCAGGCA GAGGAGCTAG CAGCCAAAGA TCACGACTCC	660
TGCGCAGGAC TGGAGGGGAG AGCTGAAGGG CAAGGAGGAG TGGATGTCGT GCTAAGGACC	720
CAGGAAGCTG TTGCTGAGGA AGATCCCATA WTGGCAGAAA AGTTCAGGGA GGAAGCGGTG	780
GATGAGGACC CAGAGGAGGA AGAGGACAAA GAGTGCAATC TGGAGACAGA AGCGATGCAG	840

GACAGGAACT	CGGAAGGGGA	CGGGGACATG	GAAGGAGAAG	GAAACACACA	AAAGAATGAG	900
GGCATGGGAG	GAGGAAGGGT	TGTGGCTGTG	GAAGTTCTAC	ACGGAGGTGG	TGAAACGGCA	960
GAAACAGCCG	CAGAGGAGAG	GGAGGTGTTG	GCAGGTTTCG	AGACAGCCGA	GGAGAAAACA	1020
ATAGCAAATA	AAGCCTCCTC	CTTTTCAGAT	GTTGCTGAGG	AAGAAACCTG	GCACCAACAG	1080
GATGAGTTAG	TAGGAAAAAC	AGCAGCTGCA	GGGAAGGTGG	TGGTAGAGGA	ATTAGCACGG	1140
AGTGGGGAGG	AAGTGCCAGC	AGCAGAGGAG	ATGACAGTGA	CATATACAAC	AGAGGCTGGG	1200
GTGGGCACTC	CAGGAGCCCT	GGAGCGGAAG	ACCTCAGGGC	TAGGACAGGA	GCAAGAGGAA	1260
GGGTCAGAGG	GCCAGGAGGC	AGCCACTGGG	AGTGGCGATG	GGAGGCAGGA	GACAGGAGCA	1320
GCTGAAAAAT	TCCGATTAGG	ATTATCACGG	GAGGGAGAGA	GGGAATTGAG	TCCGGAGAGT	1380
CTACAGGCGA	TGGCAACACT	TCCAGTGAAG	CCTGATTTC	CTGAAACCCG	AGAGAAGCAA	1440
CAGCATATGG	TGCAAGGAGA	AAGCGAGACT	GCAGATGTTT	CCCCCAACAA	CATGCAGGTC	1500
TAGGAGACTT	GCTGGCAGAC	GGATAATTTA	AAGATGTCTT	CTGAAGATGT	AAAGAGTGGA	1560
GAAAGATTCA	CGCAAGCATC	TCACCAGGAT	TCTTGATTTT	CTCTCTCTCC	TCTTTAGTTG	1620
CTGGTTGCGC	TTGTCTGAGA	TGATJCCCAA	TCTGTCAGCC	CTGGTCAGTA	GCTCAGTAAG	1680
CACCTTGAGA	ATAGCTCAAG	TAGATCTGTA	GGACCCTTCT	TAGAAGCAGT	GGTTCCTCAT	1740
GGAGAACTT	GTGAGGCTGT	TACACATTCT	ACACACCTAA	CATTATTTTC	AAACAAAAAT	1800
GATAATTTTC	AGATGCTTGA	CTTTTACCAA	AGATCACTGG	AAGGCCCAGT	CCTAATGTTA	1860
GGGGTTTGTT	TAAAGTCCTT	TTTATTTTAC	AATACAGAGC	CCCAGTCAAT	TCCACAATCT	1920
CAATTTCATA	CATGGGAATT	TTATTTAAAA	ATCTGTGGTT	TGGGGCTTTA	ATGAATTGGC	1980
CTGTGAAAAT	GAGCTCTAAA	TTTCCTCCCA	CGTACACTCA	AAACTCAAGA	TTGCTCCAAA	2040
TCTCTAAGTT	CTTCCAGCAA	AAGATTTCTT	GGCATGTATA	TTCACCTATA	CTTAGAAATA	2100
TTCATTCTTT	TAATTTATGC	CAGAATAACA	AAGTGGAAT	CTTATTTCAA	AATGCTCTTT	2160
GTTTTTTTGT	GTGTGTTTCT	GTAGTTCTGC	TTTCTGGGGT	AGACTAGTAA	AATGGTAGCT	2220
TCCAGCATTT	TGTCCCTGGG	GCCTTCTTTA	TAGGGCCACT	CAAATTTAAA	TAAAAGTAGT	2280
AAATAATTTA	GCTAAGTGGA	ATAAGTATAA	TAATTATAGT	GGTAAGCATA	GCACATCAGC	2340
ATTATGCCAA	CATTCTAGAC	TCTTTAGTTG	ATGTCATTAA	ATGGAAAAGA	AACCTGGATT	2400
AAATGAGTGT	GCTGCTCACC	TTCCCAAGTT	CTGTTATTTT	AAACCTGTGA	ACTAACCTTG	2460
CAGTTCATTA	TAAATCAACA	GTAACAACCTG	CATTCTAAAT	TACTCCCTGA	TATTATTTTC	2520

TAGTTGTGTA TCAGCCTGTC TCCTAGGGGT TTTCATTTCC CTGAAGACAT ACAAGTGCCC	2580
CAGAGCGCAT GTATATGTCT ACCATTTCTC TATATGAGAA GGTAAAAAAA ATTTCTTTAA	2640
GCAGTGATTT TCCAGCCAGA ATATACATTA GATTTTCATG GGACGCTTTT ATAAATGACT	2700
CAACCCCTTTT CCCCACCCCA GAGATTCAGA CTTAATTCGT TTTAGATGGA TCTACACATC	2760
AGTATATATA TATTTTAAAC TTTTCACTTG ATTCTTCTCT GTAGCCAAGG TTGAGAACCG	2820
CTGTTCTAAA TCATCATATA ATCCATGCTG GCCACATTAC ACTCAAGGTC CCTAGGGACC	2880
AGGCATATTA TCATAGTAGG TATCTTCCAT TTAAATGTGT AATGGAGCCA TTCAATGATC	2940
AAAAATACAC TGGACCAGAT AGTAGACTGG TCCCTTGATC AGAAGCATCA GCACATCAGC	3000
ATCACCTGGA AATTGTTCCC AGCCTTTGTC TCCTACCTAC TAAATTAGAA ACTCTTGGTG	3060
GGTTCAGTA ATCCATAGCT TAACAAGCCC TGCAGTTAAT ACTGATGTAC ACTGATGTCC	3120
AAAAACTGCT GTCATGGACT ATTGATTGTA TTGAGGATTA GTCTCAGTTG GAAAGCCAAC	3180
TACAGAGGCA TTTTGAACCT TCTTTCTTTG CCTCTCTATG TCTCTCTGTC TTTTCTGTGTC	3240
TTCTGATTTA TCTGTCTTTC TTTCTCTAGT AAATGGCACT CAATATAAAA GTGGTGGAGT	3300
CAATCTTAAA CTTATTTTTA TTATGATTGT ATTGATACAT GCACGAAGTC CCTCTGCCCT	3360
ACTCCCTATT CAAGGATATT ACTCACTGCA CATCATAAAT CTCCATCATC TGTCTTAAAG	3420
TTTTATGAGT AGATTTTCATC TACATTATAT TCAAGTTCAT TTATTACTGA GCTGTATTAC	3480
TGTGGAGCTC TAACAGTATT TGTTTCCTGA TTTCAAATC AATGCTACAG AGCAC'TTTGA	3540
ATACATCACA CCTTATAGGA AAGATAGTAA ATGTATTAAT CCCATTGAAA AATTAGTTTT	3600
GTACAATGTG CTAAATAGTA TTGCATTGGA TTACTTTTAT ATTTAACACA CTCCATCAAA	3660
ACATCCCATA ACATAATTTT ACAATCTGCA TGTGAATTTA ACTGTGAAAT TCAGTATTGT	3720
GATATTTTGA ATAAGTGAAT TCTTTCTCTG CAAATACTAT GTTGATAAAA TTACTTGTAT	3780
GTTCCCCTGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3840
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGA	3899

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met	Ile	Gly	Lys	Lys	Phe	Tyr	Pro	Arg	Glu	Leu	Asp	Leu	Ala	Arg	Glu	1	5	10	15
Arg	Arg	Lys	Ala	Glu	Arg	Pro	Lys	Thr	Ser	Leu	Arg	Lys	Thr	Asp	Ser	20	25	30	
Glu	Arg	Glu	Glu	Val	Thr	Arg	Ala	Asn	Ala	Leu	Lys	Asp	Glu	Asp	Ala	35	40	45	
Phe	Lys	Glu	Glu	Gln	Lys	Leu	Lys	Ala	Glu	Glu	Gly	Glu	Thr	Glu	Thr	50	55	60	
Glu	Val	Arg	Ala	Glu	Glu	Glu	Thr	Lys	Ala	Pro	Pro	Asn	Glu	Met	Gly	65	70	75	80
Ser	Asp	Ala	Glu	Asn	Glu	Xaa	Pro	Val	Glu	Ala	Ser	Glu	Leu	Ser	Asp	85	90	95	
Asn	Pro	Gly	Leu	Leu	Gly	Glu	Xaa	Ser	Leu	Lys	Glu	Thr	Val	Val	Pro	100	105	110	
Ile	Phe	Glu	Ala	Thr	Pro	Gly	Phe	Glu	Lys	Ser	Leu	Glu	Asn	Ile	Thr	115	120	125	
Ala	Leu	Arg	Lys	Glu	Gly	Gly	Gly	Glu	Arg	Leu	Ser	Glu	Ala	Arg	Asp	130	135	140	
Thr	Glu	His	Lys	Asp	Arg	Glu	Glu	Leu	Ser	Ser	Arg	Glu	Asn	Arg	Ala	145	150	155	160
Leu	Lys	Glu	Gly	His	Arg	Gln	Asp	Gly	Glu	Gly	Ala	Leu	Ala	Ala	Pro	165	170	175	
Glu	Ala	Glu	Pro	Ala	Gly	Lys	Val	Gln	Ala	Pro	Glu	Gly	Leu	Ile	Pro	180	185	190	
Ala	Thr	Gly	Gln	Ala	Glu	Glu	Leu	Ala	Ala	Lys	Asp	His	Asp	Ser	Cys	195	200	205	
Ala	Gly	Leu	Glu	Gly	Arg	Ala	Glu	Gly	Gln	Gly	Gly	Val	Asp	Val	Val	210	215	220	
Leu	Arg	Thr	Gln	Glu	Ala	Val	Ala	Glu	Glu	Asp	Pro	Ile	Xaa	Ala	Glu	225	230	235	240
Lys	Phe	Arg	Glu	Glu	Ala	Val	Asp	Glu	Asp	Pro	Glu	Glu	Glu	Glu	Asp	245	250	255	
Lys	Glu	Cys	Xaa	Leu	Glu	Thr	Glu	Ala	Met	Gln	Asp	Arg	Asn	Ser	Glu	260	265	270	
Gly	Asp	Gly	Asp	Met	Glu	Gly	Glu	Gly	Asn	Thr	Gln	Lys	Asn	Glu	Gly	275	280	285	

Met Gly Gly Gly Arg Val Val Ala Val Glu Val Leu His Gly Gly Gly
 290 295 300

Glu Thr Ala Glu Thr Ala Ala Glu Glu Arg Glu Val Leu Ala Gly Ser
 305 310 315 320

Glu Thr Ala Glu Glu Lys Thr Ile Ala Asn Lys Ala Ser Ser Phe Ser
 325 330 335

Asp Val Ala Glu Glu Glu Thr Trp His Gln Gln Asp Glu Leu Val Gly
 340 345 350

Lys Thr Ala Ala Ala Gly Lys Val Val Val Glu Glu Leu Ala Arg Ser
 355 360 365

Gly Glu Glu Val Pro Ala Ala Glu Glu Met Thr Val Thr Tyr Thr Thr
 370 375 380

Glu Ala Gly Val Gly Thr Pro Gly Ala Leu Glu Arg Lys Thr Ser Gly
 385 390 395 400

Leu Gly Gln Glu Gln Glu Glu Gly Ser Glu Gly Gln Glu Ala Ala Thr
 405 410 415

Gly Ser Gly Asp Gly Arg Gln Glu Thr Gly Ala Ala Glu Lys Phe Arg
 420 425 430

Leu Gly Leu Ser Arg Glu Gly Glu Arg Glu Leu Ser Pro Glu Ser Leu
 435 440 445

Gln Ala Met Ala Thr Leu Pro Val Lys Pro Asp Phe Thr Glu Thr Arg
 450 455 460

Glu Lys Gln Gln His Met Val Gln Gly Glu Ser Glu Thr Ala Asp Val
 465 470 475 480

Ser Pro Asn Asn Met Gln Val
 485

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CATTGCTAGA CAGACTCTCT TGCTTGGATG GTACTCCACC ACTTCTTGG CACATGAGAT 60

GCAAGATTGC TCAGGGTGCA GCTAATGGCA TCAATTTTCT ACATGAAAAT CATCATATTC 120

ATAGAGATAT TAAAAGTGCA AATATCTTAC TGGATGAAGC TTTTACTGCT AAAATATCTG 180
 ACTTTGGCCT TGCACGGGCT TCTGAGAAAGT TTTGCCCAGA CAGTCATGAC TAGCAGAATT 240
 GTGGGAACAA CAGCTTATAT GGCACCAGAA GCTTTGCGTG GAGAAATAAC ACCCAAATCT 300
 GATATTTACA GCTTTGGTGT GGTTTTACTA GAAATAATAA CTGGACTTCC AGCTGTGGAT 360
 GAACACCGTG AACCTCAGTT ATTGCTAGAT ATTAAAGAAG AAATTGAAGA TGAAGAAAAG 420
 ACATTGAAGA TTATATTGAT AAAAAGATGA ATGATGCTGA TTCCAATTCA GTTGAAGCTA 480
 TGT 483

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ala Ser Ile Phe Tyr Met Lys Ile Ile Ile Phe Ile Glu Ile Leu
 1 5 10 15
 Lys Val Gln Ile Ser Tyr Trp Met Lys Leu Leu Leu Leu Lys Tyr Leu
 20 25 30
 Thr Leu Ala Leu His Gly Leu Leu Arg Ser Phe Ala Gln Thr Val Met
 35 40 45
 Thr Ser Arg Ile Val Gly Thr Thr Ala Tyr Met Ala Pro Glu Ala Leu
 50 55 60
 Arg Gly Glu Ile Thr Pro Lys Ser Asp Ile Tyr Ser Phe Gly Val Val
 65 70 75 80
 Leu Leu Glu Ile Ile Thr Gly Leu Pro Ala Val Asp Glu His Arg Glu
 85 90 95
 Pro Gln Leu Leu Leu Asp Ile Lys Glu Glu Ile Glu Asp Glu Glu Lys
 100 105 110
 Thr Leu Lys Ile Ile Leu Ile Lys Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```
AATCTGAGTC AGCTTAGAAG ATANTCCAAG CTTGAGATGA TAACCACAGC CTGGGCTGAC      60
ACCTGGATTT CAGCTTTGCA TGATCCTCAG TATGAGAATC TATCTGTTCT GTGCTGGACT      120
TCTAATATAT AGAACTGTGA GATAATGGGT CACATTGGCT GGATGTGGTG GCTCATACCT      180
GTAAATCCCA GCACTTTGGG AGGCCGAGGC AGGCAGATCA CCTGAGGTCA GGAGTTCAAG      240
ACCGGCCTGG CCAGCATGGT GAAGCCCCGT CTTTACTAGA AATACAAAAA TTAGACGAGC      300
GTGGTGGTGG ACACCTGTGT TCCCAGCTAC TTGGGAGGCT GAGGCAGGAG ACTGGCTGGA      360
ACCAGGGAGG TAGAGGTTGC AGTGAGCTGA GATCGTGCCA CTGCACTCCA GCCTGGGTGA      420
CAGAGTGAGA CTCCATCATA AATAAATAAA TAAATAAATG GGTCACATTA AGCCTTTAAA      480
AAAAAAAAAA AAA                                     493
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(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```
GGTTCACAGA AGAGTTTGCG ACGTGGTAAA GAAATAAGGC GAGTACACAA GCGAAGACTT      60
TCCAGCTCAG AGAGTGAAGA GAGCTATTTG TCCAAGAAGT CTGAAGATGA TGAGCTAGCT      120
AAAGAATCAA AGCGGTCAGT TCGAAAGCGG GGCCGAAGCA CAGACGAGTA TTCAGAAGCA      180
GATGAGGAGG AGGAGGAAGA RGAAGGCAAA CCATCCCGCA AACGGCTACA CCGGATTGAG      240
ACGGATGAGG ARGAGAGTTG TGACAATGCT CATGGAGATG CAAATCAGCC TGCCCGTGAC      300
AGCCAGCCTA GGGTCCTGCC CTCAGAACAA GAGAGCACCA AGAAGCCCTA CCGGATAGAA      360
AGTGATGAGG AAGAGGACTT TGAAAATGTA GGCAAAGTGG GGAGCCCATT GGACTATAGC      420
TTAGTGGAAT TACCTTCAAC CAATGGACAG AGCCCTGGCA AAGCCATTGA GAACTTGATT      480
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GGCAAGCCTA	CTGAGAAGTC	TCAGACCCCC	AAGGACAACA	GCACAGCCAG	TGCAAGCCTA	540
GCYTCCCAAT	GGGACAAGTG	GTGGGCAGGA	GGCAGGAGCA	CCAGAAGAGG	AGGAAGATGA	600
GCTTTTGAGA	GTGACTGACC	TTGTTGATTA	TGTCTGTAAC	AGTGAACAGT	TATAAGACTT	660
TTTTTCCATT	TTTGTGCTAA	TTTATTCCAC	GGTAGCTCTC	ACACCAGCGG	GCCAGTTATT	720
AAAAGCTGTT	TAATTTTTTCC	TAGAAAACTC	CACTACAGAA	TGACTTTTAG	AAGAAAAATT	780
TCAACAAATC	CTGAAGTCTT	TCTGTGAAGT	GACCAGTTCT	GAACTTTGAA	GATAAATAAT	840
TGCTGTAAAT	TCCTTTTGAT	TTTCTTTTTC	CAGGTTTCATG	GTCCTTGGTA	ATTTCAATTCA	900
TGGAAAAAAA	TCTTATTATA	ATAACAACAA	AGATTGTAT	ATTTTTGACT	TTATATTTCC	960
TGAGCTCTCC	TGACTTTGTG	AAAAAGGGTG	ATGAAAATGC	ATTCCGAATC	TGTGAGGGCC	1020
CAAAACAGAA	TTTAGGGGTG	GGTGAAAGCA	CTTGTGCTTT	AGCTTTTTCA	TATTAAATAT	1080
ATATTATATT	TAAACATTCA	TGGCATAGAT	GATGATTTAC	AGACAATTTA	AAAGTTCAAG	1140
TCTGTACTGT	TACAGTTTGA	GAATTGTAGA	TAACATCATA	CATAAGTCAT	TTAGTAACAG	1200
CCTTTGTGAA	ATGAACTTGT	TTACTATTGG	AGATAACCAC	ACTTAATAAA	GAAGAGACAG	1260
TGAAAGTACC	ATCATAATTA	ACCTAAATTT	TTGTTATAGC	AGAGTTTCTT	GTTTAAAAAA	1320
AAAWAAAWG	CRKCYGMAAA	GCATTTGTAC	AGTAAAATGT	ATAATGAAGC	TTTGCCAACC	1380
AGACTGTGCT	AGCAACAAAT	TTTTTTTAAAT	AAGCTTTATG	CAGTGGAAT	AAGGTGGCCT	1440
CAAATATATT	GTGTCTGATG	GAGAGTTATT	AGTGAAATGA	ATGTGGTCTT	TCTTAAGGCC	1500
TGGGTGGACT	GTAAACTTTG	CCAATAGTAT	AACTCTTGTC	TTCTGGCCAC	TTGATGTTTA	1560
AATATCTGAA	ATATCATTTT	GAAAAAATA	CATCTATATA	TAACATACAT	GAAGAGATGC	1620
TAAGCTGACA	GTGATATTTT	AGCACATTTG	AAGACTGGGA	AGAGATTTTC	AGGTGAATTT	1680
TAAGTGGTCT	ATTCTTGCCC	TTAGTATCTA	CTTCAAATTG	AAGTCTACAA	ACAAAGCAGT	1740
TCCTTTGGGA	GGTTTTTAGT	TTGAGTTTTA	GCGTGTGTGT	GTGTTTGTGT	GTGTGCGTGT	1800
GCGTGTGTGT	GTGTGTTGGA	ATTCCTATC	TGCCTGGATA	TATTAGCAGA	GTTTGAATGT	1860
AGTTTTGGCC	TTTGGCCATT	AGACTTCTAT	TAAAATTCAT	TAATAGTCAT	ACAACCAACA	1920
TAGAGTTGAA	TGAGAACTGC	CGATGTAATT	AATAGGCATG	ACATCCATTT	CAAACATCTC	1980
AACACTTTAA	AGAAAAGCCC	TTTGTTTCAA	GAAAAAAGGG	TTTGTAACATA	ACTAAATACC	2040
TAACATGTAA	TTGACACTAA	AATATGAACT	TTGTCTTATT	TAGTTTCTGT	TATAGCTGTA	2100
AAATTTTCAGG	CAGAGCCATA	ACATTGTACA	GAGTGTAGCA	CTTGTGATTA	AACCTAGCCT	2160
GTAAATCCT	GAAACCTTCA	ACCATTACTT	CTGTGAATAC	TTTAGCCCTG	GGATTTGGGT	2220

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TTTTCTGTTC CGGTGTTGTG TCTGTTGCCG GCAATGGACA CACCATATCT GCTGCTGGCC      2280
CAAGGAACGT CATTAATTTT TCTTTCCAAA TTAAGTATTA TGTGCTAGTC AGTGTATAGT      2340
AAAGCACTTC TCTTTTTTAT TACTAAAAAG CTGGCATTAG ATTTGCATTA TAAATACCTC      2400
TCTAGGAACT TTATACTCCT TTCCTTCTT CAACAGGTAT TGCCCTTAAA TCTTATCTTT      2460
TGGCCTTGAA AGTTTATAGC TATTGTTTTT CAGTTGTTTCG TTGTTTTGTT TTGTTTCACT      2520
TTAGTTCTGT AGTACCTGCC CATTAATATT TTTGCTTTGA TTCTAGCAAT GTGTATGTAT      2580
CTGTATAAAA AATAAAATAA TGAAAGCAAC CTAAAAATAG GATGCACCAA TTAAAAAAA      2640
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                          2682

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(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

Met Glu Lys Asn Leu Ile Ile Ile Thr Thr Lys Ile Cys Ile Phe Leu
 1              5              10              15
Thr Leu Tyr Phe Leu Ser Ser Pro Asp Phe Val Lys Lys Gly Asp Glu
          20              25              30
Asn Ala Phe Arg Ile Cys Glu Gly Pro Lys Gln Asn Leu Gly Val Gly
          35              40              45
Glu Ser Thr Cys Ala Leu Ala Phe Ser Tyr
 50              55

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(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCCGAGCGCC CGCGCCGCCG CTGCCTCTGT CCTCCGCGCG CTGCTCAGCT GAAGGCGCAC 60
 AGGATTCAAT TACTGGACTT GTCAACTCTG CCAGTGACG TGCCATTTCT CTTCCACTAT 120
 GAGAGGACCG ATTGTATTGC ACATTTGTCT GGCTTTCTGT AGCCTTCTGC TTTTCAGCGT 180
 TGCCACACAA TGTCTGGCCT TCCCCAAAAT AGAAAGGAGG AGGGAGATAG CACATGTTCA 240
 TGCGGAAAAA GGGCAGTCCG ATAAGATGAA CACCGATGAC CTAGAAAATA GCTCTGTTAC 300
 CTCAAAGCAG ACTCCCCAAC TGGTGGTCTC TGAAGATCCA ATGATGATGT CAGCAGTACC 360
 ATCGGCAACA TCATTAAATA AAGCATTCTC GATTAACAAA GAAACCCAGC CTGGACAAGC 420
 TGGGCTCATG CAAACAGAAC GCCCTGGTGT TTCCACACYT ACTGAGTCAG GTGTCCCCCTC 480
 AGCTGAAGAA GTATTTGGTT CCAGCCAGCC AGAGAGAATA TCTCCTGAAA GTGGACTTGC 540
 CAAGGCCATG TTAACCATTG CTATCACTGC GACTCCTTCT CTGACTGTTG ATGAAAAGGA 600
 GGAACTCCTT ACAAGCACTA ACTTTCAGCC CATTGTAGAA GAGATCACAG AAACCACAAA 660
 AGGTTTTCTG AAGTATATGG ATAATCAATC ATTTGCAACT GAAAGTCAGG AAGGAGTTGG 720
 TTTGGGACAT TCACCTTCAT CCTATGTGAA TACTAAGGAA ATGCTAACCA CCAATCCAAA 780
 GACTGAGAAA TTTGAAGCAG ACACAGACCA CAGGACAAC TCTTTTCCTG GTGCTGAGTC 840
 CACAGCAGGC AGTGAGCCTG GAAGCCTCAC CCCTGATAAG GAGAAGCCTT CGCAGATGAC 900
 AGCTGATAAC ACCCAGGCTG CTGCCACCAA GCAACCACTC GAAACTTCCG AGTACACCCT 960
 GAGTGTTGAG CCAGAACTG ATAGTCTGCT GGGAGCCCCA GAAGTCACAG TGAGTGTCAG 1020
 CACAGCTGTT CCAGCTGCCT CTGCCTTAAG TGATGAGTGG GATGACACCA AATTAGAGAG 1080
 TGTAAGCCGG ATAAGGACCC CCAAGCTTGG AGACAATGAA GAGACTCAGG TGAGAACGGA 1140
 GATGTCTCAG ACAGCACAAG TAAGCCATGA GGGTATGGAA GGAGGCCAGC CTTGGACAGA 1200
 GGCTGCACAG GTGGCTCTGG GGCTGCCTGA AGGGGAAACA CACACGGGCA CAGCCCTGCT 1260
 AATAGCGCAT GGGAATGAGA GATCACCTGC TTCTACTGAT CAAAGTTCCT TTACCCCCAC 1320
 AAGTCTGATG GAAGACATGA AAGTTTCCAT TGTGAACTTG CTCAAAGTA CGGGAGACTT 1380
 CACGGAATCC ACCAAGGAAA ACGATGCCCT GTTTTTCTTA GAAACCACTG TTTCTGTCTC 1440
 TGTATATGAG TCTGAGGCAG ACCAACTGTT GGGAAATACA ATGAAAGACA TCATCACTCA 1500
 AGAGATGACA ACAGCTGTTC AAGAGCCAGA TGCCACTTTA TCCATGGTGA CACAAGAGCA 1560
 GGTGCTACC CTCGAGCTTA TCAGAGACAG TGGCAAGACT GAGGAAGAAA AGGAGGACCC 1620
 CTCTCCTGTG TCTGACGTTT CTGGTGTTAC TCAGCTGTCA AGAAGATGGG AGCCTCTGGC 1680
 CACTACAATT TCAACTACAG TCGTCCCTTT GTCTTTTGAA GTTACTCCCA CTGTGGAAGA 1740

ACAAATGGAC ACAGTCACAG GGCCAAATGA GGAGTTCACA CCAGTTCTGG GATCTCCAGT 1800
GACACCTCCT GGAATAATGG TGGGGGAACC CAGCATTTC CCTGCACTTC CTGCTTTGGA 1860
GGCATCCTCT GAGAGAAGAA CTGTTGTTCC ATCTATTACT CGTGTTAATA CAGCTGCCTC 1920
ATATGGCCTG GACCAACTTG AATCTGAAGA GGGACAAGAA GATGAGGATG AAGAGGATGA 1980
AGAAGATGAA GATGAAGAAG AGGAAGATGA GGAAGAAGAT GAGGAAGATA AAGATGCAGA 2040
CTCGCTGGAT GAGGGCTTGG ATGGTGACAC TGAGCTGCCA GGTTTTACCC TCCCTGGTAT 2100
CACATCCCAG GAACCAGGCT TAGAGGAGGG AAACATGGAC CTGTTGGAGG GAGCTACCTA 2160
CCAGGTGCCA GATGCCYTCG AGTGGGAACA GCAGAATCAA GGCCTGGTGA GAAGCTGGAT 2220
GGAAAAATTM AAAGACAAGG CTGGTTACAT GTCTGGGATG CTGGTGCCTG TAGGGGTTGG 2280
GATAGCTGGA GCCTTGTTCA TCTTGGGAGC CCTCTACAGC ATTAAGGTTA TGAATCGCCG 2340
AAGGAGAAAT GGCTTCAAAA GGCATAAAAG AAAGCAGAGA GAATTCAACA GCATGCAAGA 2400
TCGAGTAATG CTCTTAGCCG ACAGCTCTGA AGATGAATTT TGAATTGGAC TGGGTTTTAA 2460
TTGGGATATT CAACGATGCT ACTATTCTAA TTTTATTTT GGAGCAGAAA AAAAAAAAAA 2520
AA 2522

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Arg Gly Pro Ile Val Leu His Ile Cys Leu Ala Phe Cys Ser Leu
1 5 10 15
Leu Leu Phe Ser Val Ala Thr Gln Cys Leu Ala Phe Pro Lys Ile Glu
20 25 30
Arg Arg Arg Glu Ile Ala His Val His Ala Glu Lys Gly Gln Ser Asp
35 40 45
Lys Met Asn Thr Asp Asp Leu Glu Asn Ser Ser Val Thr Ser Lys Gln
50 55 60
Thr Pro Gln Leu Val Val Ser Glu Asp Pro Met Met Met Ser Ala Val
65 70 75 80

Pro Ser Ala Thr Ser Leu Asn Lys Ala Phe Ser Ile Asn Lys Glu Thr
85 90 95

Gln Pro Gly Gln Ala Gly Leu Met Gln Thr Glu Arg Pro Gly Val Ser
100 105 110

Thr Xaa Thr Glu Ser Gly Val Pro Ser Ala Glu Glu Val Phe Gly Ser
115 120 125

Ser Gln Pro Glu Arg Ile Ser Pro Glu Ser Gly Leu Ala Lys Ala Met
130 135 140

Leu Thr Ile Ala Ile Thr Ala Thr Pro Ser Leu Thr Val Asp Glu Lys
145 150 155 160

Glu Glu Leu Leu Thr Ser Thr Asn Phe Gln Pro Ile Val Glu Glu Ile
165 170 175

Thr Glu Thr Thr Lys Gly Phe Leu Lys Tyr Met Asp Asn Gln Ser Phe
180 185 190

Ala Thr Glu Ser Gln Glu Gly Val Gly Leu Gly His Ser Pro Ser Ser
195 200 205

Tyr Val Asn Thr Lys Glu Met Leu Thr Thr Asn Pro Lys Thr Glu Lys
210 215 220

Phe Glu Ala Asp Thr Asp His Arg Thr Thr Ser Phe Pro Gly Ala Glu
225 230 235 240

Ser Thr Ala Gly Ser Glu Pro Gly Ser Leu Thr Pro Asp Lys Glu Lys
245 250 255

Pro Ser Gln Met Thr Ala Asp Asn Thr Gln Ala Ala Ala Thr Lys Gln
260 265 270

Pro Leu Glu Thr Ser Glu Tyr Thr Leu Ser Val Glu Pro Glu Thr Asp
275 280 285

Ser Leu Leu Gly Ala Pro Glu Val Thr Val Ser Val Ser Thr Ala Val
290 295 300

Pro Ala Ala Ser Ala Leu Ser Asp Glu Trp Asp Asp Thr Lys Leu Glu
305 310 315 320

Ser Val Ser Arg Ile Arg Thr Pro Lys Leu Gly Asp Asn Glu Glu Thr
325 330 335

Gln Val Arg Thr Glu Met Ser Gln Thr Ala Gln Val Ser His Glu Gly
340 345 350

Met Glu Gly Gly Gln Pro Trp Thr Glu Ala Ala Gln Val Ala Leu Gly
355 360 365

Leu Pro Glu Gly Glu Thr His Thr Gly Thr Ala Leu Leu Ile Ala His
370 375 380

Gly	Asn	Glu	Arg	Ser	Pro	Ala	Phe	Thr	Asp	Gln	Ser	Ser	Phe	Thr	Pro	385	390	395	400
Thr	Ser	Leu	Met	Glu	Asp	Met	Lys	Val	Ser	Ile	Val	Asn	Leu	Leu	Gln	405	410	415	
Ser	Thr	Gly	Asp	Phe	Thr	Glu	Ser	Thr	Lys	Glu	Asn	Asp	Ala	Leu	Phe	420	425	430	
Phe	Leu	Glu	Thr	Thr	Val	Ser	Val	Ser	Val	Tyr	Glu	Ser	Glu	Ala	Asp	435	440	445	
Gln	Leu	Leu	Gly	Asn	Thr	Met	Lys	Asp	Ile	Ile	Thr	Gln	Glu	Met	Thr	450	455	460	
Thr	Ala	Val	Gln	Glu	Pro	Asp	Ala	Thr	Leu	Ser	Met	Val	Thr	Gln	Glu	465	470	475	480
Gln	Val	Ala	Thr	Leu	Glu	Leu	Ile	Arg	Asp	Ser	Gly	Lys	Thr	Glu	Glu	485	490	495	
Glu	Lys	Glu	Asp	Pro	Ser	Pro	Val	Ser	Asp	Val	Pro	Gly	Val	Thr	Gln	500	505	510	
Leu	Ser	Arg	Arg	Trp	Glu	Pro	Leu	Ala	Thr	Thr	Ile	Ser	Thr	Thr	Val	515	520	525	
Val	Pro	Leu	Ser	Phe	Glu	Val	Thr	Pro	Thr	Val	Glu	Glu	Gln	Met	Asp	530	535	540	
Thr	Val	Thr	Gly	Pro	Asn	Glu	Glu	Phe	Thr	Pro	Val	Leu	Gly	Ser	Pro	545	550	555	560
Val	Thr	Pro	Pro	Gly	Ile	Met	Val	Gly	Glu	Pro	Ser	Ile	Ser	Pro	Ala	565	570	575	
Leu	Pro	Ala	Leu	Glu	Ala	Ser	Ser	Glu	Arg	Arg	Thr	Val	Val	Pro	Ser	580	585	590	
Ile	Thr	Arg	Val	Asn	Thr	Ala	Ala	Ser	Tyr	Gly	Leu	Asp	Gln	Leu	Glu	595	600	605	
Ser	Glu	Glu	Gly	Gln	Glu	Asp	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Asp	Glu	610	615	620	
Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Asp	Lys	Asp	Ala	625	630	635	640
Asp	Ser	Leu	Asp	Glu	Gly	Leu	Asp	Gly	Asp	Thr	Glu	Leu	Pro	Gly	Phe	645	650	655	
Thr	Leu	Pro	Gly	Ile	Thr	Ser	Gln	Glu	Pro	Gly	Leu	Glu	Glu	Gly	Asn	660	665	670	
Met	Asp	Leu	Leu	Glu	Gly	Ala	Thr	Tyr	Gln	Val	Pro	Asp	Ala	Xaa	Glu	675	680	685	

Trp Glu Gln Gln Asn Gln Gly Leu Val Arg Ser Trp Met Glu Lys Xaa
690 695 700

Lys Asp Lys Ala Gly Tyr Met Ser Gly Met Leu Val Pro Val Gly Val
705 710 715 720

Gly Ile Ala Gly Ala Leu Phe Ile Leu Gly Ala Leu Tyr Ser Ile Lys
725 730 735

Val Met Asn Arg Arg Arg Arg Asn Gly Phe Lys Arg His Lys Arg Lys
740 745 750

Gln Arg Glu Phe Asn Ser Met Gln Asp Arg Val Met Leu Leu Ala Asp
755 760 765

Ser Ser Glu Asp Glu Phe
770

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGCAGCCGG TACCTGAAGT CCTTCAGAAG TGCACGCCGG GACCAGGATT CCGGGAGGCC	60
GACTCCTCCC TGCCCCACGA ATGCCGGGAA TTGTGGTCTC CGCCGGACGC GAGTTGTGAG	120
ACGGCCCAAG GGGCCGCGGG GTATGCTGGG ACCGCTAGCC CTTCCGGCGC GCCTCAGGAC	180
TTCGGGTCCC CTCACCCCGG GCGGATGCCC AAAGACTCCG CCTTCCCAAG AGCCCCTGCG	240
GCCGGGCGCG AAAATGGCGG CGGCGGCGAC GGCCGGGCGC TCCTGAAGCA GCAGTTATGG	300
AGCTTCCCTC AGGGCCGGGG CCGGAGCGGC TCTTTGACTC GCACCGGCTT CCGGGTGACT	360
GCTTCCTACT GCTCGTGCTG CTGCTCTACG CGCCAGTCGG GTTCTGCCTC CTCGTCCTGC	420
GCCTGTTTCT CGGGATCCAC GTCTTCCTGG TCAGCTGCGC GCTGCCAGAC AGCGTCCTTC	480
GCAGATTCGT AGTGCGGACC ATGTGTGCGG TGCTAGGGCT CGTGGCCCGG CAGGAGGACT	540
CCGGACTCCG GGATCACAGT GTCAGGGTCC TCATTTCCAA CCATGTGACA CCTTTCGACC	600
ACAACATAGT CAATTGCTT ACCACCTGTA GCACCGTGAG TGAGAGCGAG GCCGAGAGCG	660
CCACGGGGCG GTTCCCTGGG GCCCAGCTGA AGGCCCCCCT GTCCCCACTC GCGTTCCCCA	720
TGGAGGATAC TGAGCCTTAC CCCTAACCCC GATCCTCTAC CCAACATGTC AGTTTTTTTTT	780

TTCATTTTCC TCAATATTTT TCTTCTTGCT TTCTCTTCTC CTGGTTCCCA GCCTCTACTC	840
AATAGTCCCC CCAGCTTTGT GTGCTGGTCT CGGGGCTTCA TGGAGATGAA TGGGCGGGG	900
GAGTTGGTGG AGTCACTCAA GAGATTCTGT GCTTCCACGA GGCTTCCCCC CACTCCTCTG	960
CTGCTATTCC CTGAGGAAGA GGCCACCAAT GGCCGGGAGG GGCTCCTGCG CTTCAGAGTT	1020
TGACAGTTGC CTGTTATAAG GCAGGTGTGA GCTGCTGACT AGGCTGGCTG GATTCCCATC	1080
CTACTTTCTC CTTCTCTTTC TAGTTCCTGG CCATTTTCTA TCCAAGATGT GGTACAACCT	1140
CTTACCCTGC AAGTTCAGAG ACCCTGGTC TCTGTGACGG TGTCAGATGC CTCCTGGGTC	1200
TCAGAACTGC TGTGGTCACT TTTCGTCCCT TTCACGGTGT ATCAAGTGGC TTCGTCTGT	1260
TCATCGCCAA CTAGGGGAAG CGAATGAGGA GTTTGCACTC CGTGTACAAC AGCTGGTGGC	1320
CAAGGAATTG GGCCAGACAG GGACACGGCT CACTCCAGCT GACAAAGCAG AGCACATGAA	1380
GCGACAAAGA CACCCAGAT TGCGCCCCCA GTCAGCCCAG TCTTCTTTCC CTCCTCCCC	1440
TGGTCCTTCT CCTGATGTGC AACTGGCAAC TCTGGCTCAG AGAGTCAAGG AAGTTTTGCC	1500
CCATGTGCCA TTTGGTGTCA TCCAGAGAGA CCTGGCCAAG ACTGGCTGTG TAGACTTGAC	1560
TATCACTAAT CTGCTTGAGG GGGCCGTAGC TTTCATGCCT GAAGACATCA CCAAGGGAAC	1620
TCAGTCCCTA CCCACAGCCT CTGCCTCCAA GTTTCCCAGC TCTGGCCCGG TGACCCCTCA	1680
GCCAACAGCC CTAACATTTG CCAAGTCTTC CTGGGCCCGG CAGGAGAGCC TGCAGGAGCG	1740
CAAGCAAGCA CTATATGAAT ACGCAAGAAG GAGATTCA CA GAGAGACGAG CCCAGGAGGC	1800
TGACTGAGCT CAAAGGAACA GGATGGCACC CAGAGCCGCA GGACGGAGAC TGGGGGCAGC	1860
CCTCACCCAA CTCACAACAG GCTGGATGGG TGGGTGGTAA AAAGGGAAGG ATGAGGCTCC	1920
CCCAATGTCA CATTAAATTC ATGGTTTTCA TTCAAGGVAA AAAAAAAAAA AAAAAAAAAA	1980
AAAAAAAAA AAAAAAAAAA AA	2002

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Met Pro Pro Gly Ser Gln Asn Cys Cys Gly His Phe Ser Ser Leu Ser
1 5 10 15

Arg Cys Ile Lys Trp Leu Arg Pro Val His Arg Gln Leu Gly Glu Ala
20 25 30

Asn Glu Glu Phe Ala Leu Arg Val Gln Gln Leu Val Ala Lys Glu Leu
35 40 45

Gly Gln Thr Gly Thr Arg Leu Thr Pro Ala Asp Lys Ala Glu His Met
50 55 60

Lys Arg Gln Arg His Pro Arg Leu Arg Pro Gln Ser Ala Gln Ser Ser
65 70 75 80

Phe Pro Pro Ser Pro Gly Pro Ser Pro Asp Val Gln Leu Ala Thr Leu
85 90 95

Ala Gln Arg Val Lys Glu Val Leu Pro His Val Pro Phe Gly Val Ile
100 105 110

Gln Arg Asp Leu Ala Lys Thr Gly Cys Val Asp Leu Thr Ile Thr Asn
115 120 125

Leu Leu Glu Gly Ala Val Ala Phe Met Pro Glu Asp Ile Thr Lys Gly
130 135 140

Thr Gln Ser Leu Pro Thr Ala Ser Ala Ser Lys Phe Pro Ser Ser Gly
145 150 155 160

Pro Val Thr Pro Gln Pro Thr Ala Leu Thr Phe Ala Lys Ser Ser Trp
165 170 175

Ala Arg Gln Glu Ser Leu Gln Glu Arg Lys Gln Ala Leu Tyr Glu Tyr
180 185 190

Ala Arg Arg Arg Phe Thr Glu Arg Arg Ala Gln Glu Ala Asp
195 200 205

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CAATTGGGCC GCGAGTTGTG GTTTAAACCA GGAGTGC GCC GCGTCCGTTC ACCGCGGCCT 60

CAGATGAATG CGGCTGT TAA GACCTGCAAT AATCCAGAAT GGCTACTCTG ATCTATGTTG 120

ATAAGGAAAA TGGAGAACCA GGCACCCGTG TGGTTGCTAA GGATGGGCTG AAGCTGGGGT 180

CTGGACCTTC AATCAAAGCC TTAGATGGGA GATCTCAAGT TTCAACACCA CGTTTTGGCA 240
AAACGTTCTGA TGCCCCACCA GCCTTACCTA AAGCTACTAG AAAGGCTTTG GGAAGTGTCA 300
ACAGAGCTAC AGAAAAGTCT GTAAAGACCA AGGGACCCCT CAAACAAAAA CAGCCAAGCT 360
TTTCTGCCAA AAAGATGACT GAGAAGACTG TTAAAGCAAA AAGCTCTGTT CCTGCCTCAG 420
ATGATGCCTA TCCAGAAATA GAAAAATTCT TTCCCTTCAA TCCTCTAGAC TTTGAGAGTT 480
TTGACCTGCC TGAAGAGCAC CAGATTGCGC ACCTCCCCTT GAGTGGAGTG CCTCTCWTGA 540
TCCTTGACGA GGAGAGAGAG CTGAAAAGC TGTTTCAGCT GGGCCCCCCT TCACCTGTGA 600
AGATGCCCTC TCCACCATGG GAATCCAATC TGTTGCAGTC TCCTTCAAGC ATTCTGTCTGA 660
CCCTGGATGT TGAATTGCCA CCTGTTTGCT GTGACATAGA TATTTAAATT TCTTAGTGCT 720
TCAGAGTTTG TGTGTATTTG TATTAATAAA GCATTCTTTA ACAGAAAAAA AAAAAAAAAA 780
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 819

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met Ala Thr Leu Ile Tyr Val Asp Lys Glu Asn Gly Glu Pro Gly Thr
1 5 10 15
Arg Val Val Ala Lys Asp Gly Leu Lys Leu Gly Ser Gly Pro Ser Ile
20 25 30
Lys Ala Leu Asp Gly Arg Ser Gln Val Ser Thr Pro Arg Phe Gly Lys
35 40 45
Thr Phe Asp Ala Pro Pro Ala Leu Pro Lys Ala Thr Arg Lys Ala Leu
50 55 60
Gly Thr Val Asn Arg Ala Thr Glu Lys Ser Val Lys Thr Lys Gly Pro
65 70 75 80
Leu Lys Gln Lys Gln Pro Ser Phe Ser Ala Lys Lys Met Thr Glu Lys
85 90 95
Thr Val Lys Ala Lys Ser Ser Val Pro Ala Ser Asp Asp Ala Tyr Pro

100

105

110

Glu Ile Glu Lys Phe Phe Pro Phe Asn Pro Leu Asp Phe Glu Ser Phe
115 120 125

Asp Leu Pro Glu Glu His Gln Ile Ala His Leu Pro Leu Ser Gly Val
130 135 140

Pro Leu
145

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TNTCCTGCCTC AGCTGCCTCT CTGTGTAA

29

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CNCACTGCCCT CCTTCTCCCA TAGGTACT

29

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:
GNAATAAGCAT GATGCTCTAC AAGGAAAG 29

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:
TNGGTGCCATG ATTCTGAGTG CCCTTTGC 29

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:
GNATATGTCAC TGTCATCTCC TCTGCTGC 29

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:
ANAAGCTTCAT CCAGTAAGAT ATTTGCAC 29

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ANTTCAGAACT GGTCACTTCA CAGAAAGA

29

- (2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GNATTACATA GGATGAAGGT GAATGTCC

29

- (2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ANTAGAGGCTG GGAACCAGGA GAAGAGAA

29

- (2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TNTTGCAGGTC TTAACAGCCG CATTCATC

29

- (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```

Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp Ser His
1           5           10           15

Arg Leu Pro Gly Asp Cys Phe Leu Leu Val Leu Leu Leu Tyr Ala
          20           25           30

Pro Val Gly Phe Cys Leu Leu Val Leu Arg Leu Phe Leu Gly Ile His
          35           40           45

Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
          50           55           60

Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu
65           70           75           80

Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His
          85           90           95

Val Thr Pro Phe Asp His Asn Ile Val Asn Leu Leu Thr Thr Cys Ser
          100          105          110

Thr

```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

Ser Gln Pro Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg
1           5           10           15

Gly Phe Met Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys
          20           25           30

Arg Phe Cys Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe
          35           40           45

Pro Glu Glu Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe
          50           55           60

```

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

Ser Ser Trp Pro Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu
1           5           10           15

Gln Val Gln Arg Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp
                20           25           30

Val Ser Glu Leu Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln
          35           40           45

Val
  
```

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

CAGGTGGTCC TCCACCTGCC TTGGCTTCCT AAAGTGCTGG GATTACAGGC ATGAGTCACT      60

CTGCTGGCCT ATGTTCTGTT TTTGTTTTTG TTTTGTGTTT GAGACAGAGT TTTACTCTTG      120

TTGCCCAGGC TGGAGTGCAA TGGCATAATC TCGGCTCACT GCAGCCTCTG CCTCCCAGGT      180

TCAAGTGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA TTACAGGCAT GTGCCACCTC      240

ACCTGGCTAA TTTTGTATTT TTAGTAGAGA TGGGGTTTCT CCATGTTAGT CAGGCTGGTC      300

TTGAACTCCT GACCTCAGGT GATCTGCCCT CCTCAGCCTC CTAAAGTGCT GGGATTACAG      360

GTGTGAGCCA CTGTGCCCAG CCTTGTTTTT TGTTTTTTTT TTTTGTGTTT TTTTTTTGAC      420

AGTAGCCATC CTAATAGATA CTAAGTGGTA TCTCATTGTG GTTTTGATTG CATGCGTTCT      480

TTTTGGCTTG TTTTTTGAGA CAAGGTCTCA CTCCATCACC CAGACTGGAG CGCAGTGGTG      540

TGATCACGGC TCGTTGCAAC CTGACCCTCT TGAGCTCAGG TGATCCTCCC ACTTCACCCT      600

CCCGAGTATC TTGGAGTACA GGTGTGTGCC TGGCTGATTT TTCGTATTTT TTGTAGAGAT      660
  
```

GGGGTTTCAC	CGTGTGCTC	AGGCTGCTCT	CAAAGTCTG	GGCTCAAACG	ATCCTCCTGC	720
CTTGGCCTCC	CAAAGTCTG	GGGTACAAAG	CATGAACCAT	TATGCCCGGC	CTGCATGCAC	780
TCTTACACAC	GTTTTATCTG	TTACATATCC	CAAGATGTGT	AGTTCTTTGG	GAAGCAGGAA	840
GAAATGGGGG	TAACATTGAG	AAGTTAAGGA	AAAGTGGTAT	AAATTATTGG	CAGCAGCTCC	900
TGATTATAGG	TTTTGAGGCC	TGAGTCCATG	GGCAGAGTCC	CTCTCCTGCA	GTTTCATGAGA	960
TTTGTACCCT	CCAGTGACAG	TACTGGGAAG	GAGGGAATGC	TACGTTCCAA	CTCTTAGTCT	1020
TCACTTAATT	TTATGACTCA	AAATTCCAGC	TAGATATATA	GGTTACTTTT	ACTGTTGGAT	1080
CACTCTGGCC	CACGAATGTA	TCCTGCTAAC	TTGATGTGTG	CTCTAACTAC	CTCCTAAGTT	1140
TGGTGACAGT	CGGCAGAGTT	TGTGAACCAT	GTGATTCCCA	ACTTAAGTTA	CTAACATTTT	1200
TTTTTTTTTT	TTTTGAGACA	GGATCTTGCT	CTGTCACCCA	GGCTGGAGTG	CAGTGGTACG	1260
ATCTCAGCTC	ACTGTAGCCT	TAACCCACCC	AGGCTTATGT	GCTCCTCCCA	CCTCAGCCTC	1320
CCGAGTAGTT	GGAAGTATAG	GTGCATACCA	CCATGCCTGG	CTAATTTTTG	TATTTTTTGT	1380
AGAGGCAGGG	TTTTGCCCTG	TTGCCCAGGC	TGGTCTTGAA	CTCCTGAGCT	CAAGCAATCC	1440
TCCCACCTCA	GCCTCCCAA	GGGTGGGAT	TACAGGTGTG	AGCCACTGCA	CCCGGCCAAG	1500
TTACTAACAT	TTTAAGTCTA	AAGTAAAAGA	TTGCTTCTGT	ATGTTCTCCC	CCAGGTGTGT	1560
AGGTCCATCC	TGGGAAGGCC	ATCAGACACA	CCTAGTCCAT	GGGTGACACC	CAGCCAGTTT	1620
TTAATGCCAG	TTCCTCTGGC	AGTTTTTAAT	TTAGGCACTC	GGAAGTGAAA	CCCGGACATT	1680
CACTGGAAAT	GACTTTAGGA	CAAGACCTGC	TGGCCATGAG	CTGAGAAATG	TCTTACTCTC	1740
TTGCAGGGAG	AATGCTGTTG	AAAGACTTGA	TTCATTAATA	CAAGCGACTC	ACGTTGCAAT	1800
GAGAGGCAAC	TCCGATTACG	CTGATCTTAG	TGATGGCTGG	CTCGAAATAA	TACGTGTAGA	1860
TGCCCCTGAT	CCAGGTGCAG	ACCCGCTGGC	TAGCAGTGTG	AACGGCATGT	GCCTGGATAT	1920
TCCTGCTCAC	CTGAGCATCC	GCATCCTCAT	CTCGGATGCT	GGCGCGGTGG	AAGGGATTAC	1980
TCAGCAGGAG	ATACTCGGTG	TAGAGACAAG	GTTCTCCTCA	GTGAACTGGC	AGTACCAGTG	2040
TGGGCTTACC	TGTGAGCACA	AGGCCGACCT	TCTCCCTATC	AGTGCATCCG	TCCAGTTTAT	2100
TAAAATTTCCT	GCACAGTTAC	CCCACCCCTT	GACAAGATTC	CAGATCAATT	ATACAGAGTA	2160
TGACTGCAAC	AGAAATGAGG	TGTGTTGGCC	GCAGCTTCTA	TATCCATGGA	CTCAGTATTA	2220
TCAAGGGGAG	CTGCATTCTC	AGTGTGTTGC	TAAGGGCTTA	CTGTTGCTGT	TGTTCTCTAC	2280
ATTGGCCTTG	TTCCTCAGCA	ACCCCTGGAC	CAGAAATATG	AAAGCCTATA	GTTAGACAAC	2340

CACCTGGCTT TTATTTTTTT GAGATGGAGT TTTGCTCTTG TTACCCAGGC TGGAGTGCAG 2400
 TGCACAATCT CGGCTCACTG CAATCTCTGC CTCCCAAGCA ATCCTCCCAC CTCAGCCTCT 2460
 GGTGTAGCTG GGACCACAGA TGCTCCACCA TGCCTGGCTG TATTTTTTGGT AAAGATGGGG 2520
 TTTCGCCTTG TTGCCCAGGG TGGTCTGTAA CTCCTGAGCT CAGATGATCT GCCCACCTCG 2580
 GCCTCCCAAA GTGCTGGGAT CACAGACGTG AGCCACTGCG TCCGGTCCAT CTGACTTCTC 2640
 AAAGACTTTA GACCTTGACT TCAGTGATTT GTTGTAGTCT TGTATGCTTC TCTATAAAAT 2700
 TTTAATAAAT GAAATGTCTT ATTTTTGTAG AAAATTTTAA AAAAAAAAAA AAAA 2754

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Arg Gly Asn Ser Asp Tyr Ala Asp Leu Ser Asp Gly Trp Leu Glu
 1 5 10 15
 Ile Ile Arg Val Asp Ala Pro Asp Pro Gly Ala Asp Pro Leu Ala Ser
 20 25 30
 Ser Val Asn Gly Met Cys Leu Asp Ile Pro Ala His Leu Ser Ile Arg
 35 40 45
 Ile Leu Ile Ser Asp Ala Gly Ala Val Glu Gly Ile Thr Gln Gln Glu
 50 55 60
 Ile Leu Gly Val Glu Thr Arg Phe Ser Ser Val Asn Trp Gln Tyr Gln
 65 70 75 80
 Cys Gly Leu Thr Cys Glu His Lys Ala Asp Leu Leu Pro Ile Ser Ala
 85 90 95
 Ser Val Gln Phe Ile Lys Ile Pro Ala Gln Leu Pro His Pro Leu Thr
 100 105 110
 Arg Phe Gln Ile Asn Tyr Thr Glu Tyr Asp Cys Asn Arg Asn Glu Val
 115 120 125
 Cys Trp Pro Gln Leu Leu Tyr Pro Trp Thr Gln Tyr Gln Gly Glu
 130 135 140
 Leu His Ser Gln Cys Val Ala Lys Gly Leu Leu Leu Leu Phe Leu

145	150	155	160
Thr Leu Ala Leu Phe Leu Ser Asn Pro Trp Thr Arg Ile Cys Lys Ala			
	165	170	175
Tyr Ser			

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TAGGCCATGA AGGCCGTTT TTCATAAAAT AGGAATGAGG ACAAATGTTG CTCTTCATCC	60
TACCAGCTGT TTGTTCTTTG GTAGGGGATC ATGAGTGGAA AAACAAAGGC AAGAAGGGCT	120
GCCATGTTTT TTAGACGTTG CTCTGAAGAC GCCAGCGGTA GCGCCAGTGG CAATGCTTTG	180
TTATCAGAGG ACGAAAATCC TGATGCGAAT GGGGTAACTC GATCATGGAA GATTATTCTA	240
AGTACAATGC TTACACTGAC TTTTCTTCTT GTAGGACTCC TAAATCATCA GTGGCTTAAA	300
GAAACAGATG TTCCTCAGAA ATCCAGACAA TTATATGCCA TAATTGCAGA ATATGGTTCA	360
AGGCTTTATA AATATCAGGC CAGACTTCGT ATGCCTAAAG AGCAACTGGA ACTTTTAAAG	420
AAGGAAAGCC AGAATCTGGA AAACAATTTT CGTCAAATTC TATTTTTGAT CGAACAAATA	480
GATGTCCTGA AGGCATTGCT AAGAGATATG AAGGATGGTA TGGACAATAA TCACAACCTGG	540
AACACCCATG GAGACCCTGT GGAGGACCCG GACCACACAG AGGAAGTGTC AAACCTTGGTC	600
AATTATGTAC TTAAAAAGTT GAGAGAAGAC CAAGTCGAGA TGGCTGATTA TGCCCTGAAG	660
TCGGCCGAG CCTCCATCAT TGAAGCTGGG ACCTCAGAAA GTTATAAAAA TAATAAAGCA	720
AAATTGTACT GGCATGGGAT AGGTTTCCTA AATCATGAAA TGCCTCCAGA TATTATTCTT	780
CAGCCGGATG TCTACCCTGG AAAGTGCTGG GCTTTTCCAG GTTCCCAGGG TCATACCCTA	840
ATCAAGCTTT ACAAAGATCA TACCAACTGC TGTTACCATG GAGCACATCT CAGAGAAGGT	900
GTCTCCGTCA GGAAACATCT CCAGTGCACC CAAGGAATTT TCTGTCTATG GCATCACAAA	960
AAAATGTGAA GGAGAAGAAA TTTTCCTAGG TCAGTTTATA TATAACAAAA CAGGAACCAC	1020
CGTTCAAACA TTTGAACTCC AGCATGCAGT TTCTGAATAT TTATTATGTG TGAAACTTAA	1080

TATCTTTAGC AACTGGGGAC ACCCGAAGTA TACTTGTTTA TATCGATTCA GGGTCCATGG 1140
CACACCAGGC AAGCACATCT AGAAGAGTTG GTACAGAAGG CCATGCCACA TGTCCAGAAT 1200
ATTCAAGAAT GCTTATTCTC TTAGATGATA CCGCACCCAT AGGAATTGAG AATTGGGAGT 1260
GGGAAGAAAA CCTCAAAGTG GTTCATACTT GCCTGTAAAA AGTAAATGCA TTTTACTAAT 1320
AAAAAATAT GGAAGTAAAT TAAAAA AAA 1363

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met	Ser	Gly	Lys	Thr	Lys	Ala	Arg	Arg	Ala	Ala	Met	Phe	Phe	Arg	Arg	1	5	10	15
Cys	Ser	Glu	Asp	Ala	Ser	Gly	Ser	Ala	Ser	Gly	Asn	Ala	Leu	Leu	Ser	20	25	30	
Glu	Asp	Glu	Asn	Pro	Asp	Ala	Asn	Gly	Val	Thr	Arg	Ser	Trp	Lys	Ile	35	40	45	
Ile	Leu	Ser	Thr	Met	Leu	Thr	Leu	Thr	Phe	Leu	Leu	Val	Gly	Leu	Leu	50	55	60	
Asn	His	Gln	Trp	Leu	Lys	Glu	Thr	Asp	Val	Pro	Gln	Lys	Ser	Arg	Gln	65	70	75	80
Leu	Tyr	Ala	Ile	Ile	Ala	Glu	Tyr	Gly	Ser	Arg	Leu	Tyr	Lys	Tyr	Gln	85	90	95	
Ala	Arg	Leu	Arg	Met	Pro	Lys	Glu	Gln	Leu	Glu	Leu	Leu	Lys	Lys	Glu	100	105	110	
Ser	Gln	Asn	Leu	Glu	Asn	Asn	Phe	Arg	Gln	Ile	Leu	Phe	Leu	Ile	Glu	115	120	125	
Gln	Ile	Asp	Val	Leu	Lys	Ala	Leu	Leu	Arg	Asp	Met	Lys	Asp	Gly	Met	130	135	140	
Asp	Asn	Asn	His	Asn	Trp	Asn	Thr	His	Gly	Asp	Pro	Val	Glu	Asp	Pro	145	150	155	160
Asp	His	Thr	Glu	Glu	Val	Ser	Asn	Leu	Val	Asn	Tyr	Val	Leu	Lys	Lys				

175

His Lys Lys Met
290

(A) LENGTH: 2911 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

- 122 -

TAGAATATCA	GGCATGTGTC	TTAGGAAAAC	AGATCTCAGT	CAAATGTGAA	GGACATTGCC	600
CATGTCCTTC	AGATAAGCCC	ACCAGTACAA	GCAGAAATGT	TAAGAGAGCA	TGCAGTGACC	660
TGGAGTTCAG	GGAAGTGGCA	AACAGATTGC	GGGACTGGTT	CAAGGCCCTT	CATGAAAAGTG	720
GAAGTCAAAA	CAAGAAGACA	AAAACATTGC	TGAGGCCTGA	GAGAAGCAGA	TTCGATACCA	780
GCATCTTGCC	AATTTGCAAG	GACTCACTTG	GCTGGATGTT	TAACAGACTT	GATACAAACT	840
ATGACCTGCT	ATTGGACCAG	TCAGAGCTCA	GAAGCATTTA	CCTTGATAAG	AATGAACAGT	900
GTACCAAGGC	ATTCTTCAAT	TCTTGTGACA	CATACAAGGA	CAGTTTAATA	TCTAATAATG	960
AGTGGTGCTA	CTGCTTCCAG	AGACAGCAAG	ACCCACCTTG	CCAGACTGAG	CTCAGCAATA	1020
TTCAGAAGCG	GCAAGGGGTT	AAGAAGCTCC	TAGGACAGTA	TATCCCCCTG	TGTGATGAAG	1080
ATGGTTACTA	CAAGCCAACA	CAATGTCATG	GCAGTGTGTT	ACAGTGCTGG	TGTGTTGACA	1140
GATATGGAAA	TGAAGTCATG	GGATCCAGAA	TAAATGGTGT	TGCAGATTGT	GCTATAGATT	1200
TTGAGATCTC	CGGAGATTTT	GCTAGTGGCG	ATTTTCATGA	ATGGACTGAT	GATGAGGATG	1260
ATGAAGACGA	TATTATGAAT	GATGAAGATG	AAATTGAAGA	TGATGATGAA	GATGAAGGGG	1320
ATGATGATGA	TGGTGGTGAT	GACCATGATG	TATACATTTA	ATTGATGACA	GTTGAAATCA	1380
ATAAATTCTA	CATTTCTAAT	ATTTACAAAA	ATGATAGCCT	ATTTAAAAAT	ATCTTCTTCC	1440
CCAATAACAA	AATGATTCTA	AACCTCACAT	ATATTTTGTA	TAATTATTTG	AAAAAATTGCA	1500
GCTAAAGTTA	TAGAACTTTA	TGTTTAAATA	AGAATCATTT	GCTTTGAGTT	TTTATATTCC	1560
TTACACAAAA	AGAAAATACA	TATGCAGTCT	AGTCAGACAA	AATAAAGTTT	TGAAGTGCTA	1620
CTATAATAAG	TTTTTCACGA	GAACAAACTT	TGTAAATCTT	CCATAAGCAA	AATGACAGCT	1680
AGTGCTTGGG	ATCGTACATG	TTAATTTTCT	GAAAGATAAT	TCTAAGTGAA	ATTTAAAAATA	1740
AATAAATTTT	TAATGACCTG	GGTCTTAAGG	ATTTAGGAAA	AATATGCATG	CTTTAATTGC	1800
ATTTCCAAAG	TAGCATCTTG	CTAGACCTAG	TTGAGTCAGG	ATAACAGAGA	GATACCACAT	1860
GGCAAGAAAA	ACAAAGTGAC	AATTGTAGAG	TCCTCAATTG	TGTTTACATT	AATAGTGGTG	1920
TTTTTACCTA	TGAAATTATT	CTGGATCTAA	TAGGACATTT	TACAAAATGG	CAAGTATGGA	1980
AAACCATGGA	TTCTGAAAGT	TAAAAATTTA	GTTGTTCTCC	CCAATGTGTA	TTTTAATTTG	2040
GATGGCAGTC	TCATGCAGAT	TTTTTAAAAG	ATTCTTTAAT	AACATGATTT	GTTTGCCTTT	2100
CTAGATTTCT	TTATCTTTCT	GACCAGCAAC	TTAGGGAGCA	GAATTTAAAT	TAGGAAGACA	2160
AAGGGAAAAGA	TTCATTTAAA	CCATATTTTT	ACAAAGTTTG	TCATTTGCCC	CAAGGTCAAA	2220

TTTAAATTC TTAATTTTCA TTTTATTTCC CATTTTAGGT AAAAGTTTGC ATTTAATCTT 2280
 AGAATTATGT TATTTTGTGTT AGTAGTGTGG AAAGTTAGAG AACTTATTGT ATGGTGCCTT 2340
 GCAAAAATAG AGATAGAAAG ATTTTAGCAT GCATACCAAT ATAGTATATT ACGCAATATA 2400
 TAAGCACACC TAATTAACAG ATTAATATCA GTAAAGGTAT TGCTGCTGGA ATGAAGAAAA 2460
 TGGGATACGT TTGTTTCTTT TTTTCTATTG TWACATAATT GCCATGTGGA CTTGTTTATG 2520
 ATTATTGTGT AGAGTAGCAT TTAAGATTTA ACTGTAGCAA AAATTACTTT AACCGCTGTA 2580
 TTTAAGTTAG CATGTTAATT AATTGTGTAG ACATTTTGGC ACACCATCAC TTTTAACTAT 2640
 ATCATACCAA TGGTTTTGTG CCCATAATAA AAATGGAAAA ACCTGTTGAA TGTTACGTAT 2700
 TGGTATCTTT AATTTCAACA GTGGGTAAAC TGGTTTCCCA GTATACAATT CATTGAAAGC 2760
 AAAATTGATT AATTATTTCC ATTTAATTTA TACACACTCA ATACAAAATT TAATGTTGAC 2820
 TTTACGTAAT AAAGTATAAT GCATTTTCTT TTTTACTGTT TATGTATAGT TTACAAAATA 2880
 AAGAATCTTG TAACCAAAAA AAAAAAAAAA A 2911

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met	Leu	Lys	Val	Ser	Ala	Val	Leu	Cys	Val	Cys	Ala	Ala	Ala	Trp	Cys
1				5					10					15	
Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly	Gly	Arg
			20					25					30		
Ser	Asp	Gly	Gly	Asn	Phe	Leu	Asp	Asp	Lys	Gln	Trp	Leu	Thr	Thr	Ile
		35					40					45			
Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys	Phe	Arg	Asp	Glu
		50				55					60				
Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro	Gly	Lys	Pro	Phe	Asp
65					70					75				80	
Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys	Leu	Lys	Met	Lys	Cys	Ser
				85					90					95	

Arg His Lys Val Cys Ile Ala Gln Asp Ser Gln Thr Ala Val Cys Ile
100 105 110

Ser His Arg Arg Leu Thr His Arg Met Lys Glu Ala Gly Val Asp His
115 120 125

Arg Gln Trp Arg Gly Pro Ile Leu Ser Thr Cys Lys Gln Cys Pro Val
130 135 140

Val Tyr Pro Ser Pro Val Cys Gly Ser Asp Gly His Thr Tyr Ser Phe
145 150 155 160

Gln Cys Lys Leu Glu Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser
165 170 175

Val Lys Cys Glu Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser
180 185 190

Thr Ser Arg Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu
195 200 205

Val Ala Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly
210 215 220

Ser Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg
225 230 235 240

Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp Met
245 250 255

Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln Ser Glu
260 265 270

Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr Lys Ala Phe
275 280 285

Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile Ser Asn Asn Glu
290 295 300

Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro Pro Cys Gln Thr Glu
305 310 315 320

Leu Ser Asn Ile Gln Lys Arg Gln Gly Val Lys Lys Leu Leu Gly Gln
325 330 335

Tyr Ile Pro Leu Cys Asp Glu Asp Gly Tyr Tyr Lys Pro Thr Gln Cys
340 345 350

His Gly Ser Val Gly Gln Cys Trp Cys Val Asp Arg Tyr Gly Asn Glu
355 360 365

Val Met Gly Ser Arg Ile Asn Gly Val Ala Asp Cys Ala Ile Asp Phe
370 375 380

Glu Ile Ser Gly Asp Phe Ala Ser Gly Asp Phe His Glu Trp Thr Asp
385 390 395 400

Asp Glu Asp Asp Glu Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu
405 410 415

Asp Asp Asp Glu Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His
420 425 430

Asp Val Tyr Ile
435

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGATTCTGAAG TTTAAGAAAC TGCATTTTAA AGTGCCCAAA GTTTCATTTT CTTCTACCAA	60
AACTCCTAAA GATAGTTTAG TCCCAGGTGC AAAGTCTAGC ATAGGTCTTT CCACGATTCC	120
TTTATCATCT TCAGAATGCT CAAGTTTGA ATTACAACAG GTTTCGGCTT GTTCAGAGCC	180
ATCCATGCAG ATGCCTAAGG TGGGTTTTGC TGGGTTTCCA TCATCCCGGC TTGATCTCAC	240
TGGTCCTCAC TTTGAATCTT CTATTCTCTC TCCCTGTGAG GATGTTACAC TTACAAAATA	300
CCAGGTGACT GTTCCCAGA GCTGCCTTGG CCCCTGAGCT TGCTCTGGAA ATTCCTTCTG	360
GGTCTCAGGC TGATATTCCT CTTCCCAAGA CAGAGTGCTC CACTGAMCTG CAGCCTCCAG	420
ARGGAGTTCC AACATCTCAA GCTGAGAGTC ACTCTGGCCC ACTGAATTCC ATGATTCTCTG	480
TTTCTCTTGG TCAGGTGTCT TTTCTAAAT TCTATAAACC AAAGTTTGTG TTTTCAGTCC	540
CCCAAATGGC AGTTCCTGAG GGAGACCTAC ATGCAGCAGT GGGTGCCCCA GTCATGTYTC	600
YTCTTAGCCC TTGGAGAAAG AGTGCAGTGC CCCTTGCCAA GCACCCAGYT GCCATCCCCA	660
GGCACCTGTG TGTCCCAGGG CCCAGAAGAG CTTGTGGCCT CCTTGCAGAC ATCAGTAGTG	720
GCCCYTGGAG AAGCCCCTTC TGAAGATGCT GACCACGAAG GGAAAGGGAG TCCCTTGAAA	780
ATGCCTAAGA TTAAGCTTCC ATCATTTAGG TGGTCCCCGA AGAAGGAAAC AGGGCCAAAG	840
GTGGACCCAG AATGCAGCGT GGAGGACTCA AAACCTCAGCC TGGTTTTAGA CAAGGATGAA	900
GTGGCCCCGC AGTCTGCCAT CCACATGGAT CTGCCCTCTG AGAGGGATGG AGAGAAGGGG	960
AGGAGCACAA AGCCTGGCTT TGCCATGCCA AAACCTGCAC TTCCCAAAT GAAGGCTTCT	1020

AAGAGTGGGG TCAGCCTGCC ACAGAGAGAC GTGGATCCTT CCCTTTCTAG TGCCACAGCA 1080
GGGGGTAGCT TTCAAGACAC AGAAAAGGCC AGCAGTGACG GTGGTAGGGG AGGACTTGGT 1140
GCAACAGCAA GTGCCACAGG AAGTGAGGGT GTGAACCTCC ACCGGCCACA GGTCCACATT 1200
CCCAGTTTGG GCTTTGCCAA ACCTGATCTC AGATCCTCCA AGGCCAAGGT GGAGGTGAGC 1260
CAGCCTGAAG CTGACCTGCC TCTTCCCAA CATGATCTGT CTACCGAAGG TGACAGCAGA 1320
GGATGTGGGC TCGAGGATGT CCCAGTGAGC CAGCCTTG TG GGGAGGGGAT AGCCCCACA 1380
CCTGAAGATC CCCTCCAGCC ATCCTGTAGA AAACCAGATG CTGAAGTCCT CACAGTGGA 1440
AGCCCAGAGG AGGAAGCCAT GACCAAGGAC TCGCAGGAAA GCTGGTTTAA AATGCCCAAG 1500
TTCCGCATGC CCAGCCTTAG GCGCTCTTTC AGGGACAGAG GCGGGGCTGG AAAGCTGGAA 1560
GTGGCTCAGA CACAGGCACC GGCAGCAACA GGGGGTGAAG CAGCAGCTAA AGTCAAAGAG 1620
TTCCTTGTTT CTGGGTCAAA CGTGGAGGCA GCTATGTCCC TACAGCTCCC AGAGGCAGAT 1680
GCAGAAGTGA CAGCTTCTGA GAGCAAATCA TCCACAGATA TTCTAAGGTG TGATCTTGAC 1740
AGCACAGGCT TGAAGCTGCA CCTTCCACT GCTGGGATGA CTGGGGATGA GCTTCCACT 1800
TCTGAGGTCA GGATCCATCC ATCCAAAGGA CCTCTCCCTT TTCAGATGCC TGGCATGAGG 1860
CTTCCAGAAA CCCAGGTTCT TCCAGGAGAA ATAGATGAGA CTCCTCTTTC CAAGCCAGGA 1920
CATGACCTTG CCAGCATGGA GGATAAAACA GAGAAATGGT CTTCCAGCC TGAAGGTCCA 1980
CTTAAATTGA AAGCTTCAAG TACTGATATG CCATCCCAGA TTTCTGTGGT TAATGTGGAT 2040
CAACTGTGGG AAGATTCTGT CCTAACTGTC AAATTCCCCA AATTAATGGT ACCAAGGTTT 2100
TCCTTCGCTG CCCCAGCTC AGAGGATGAT GTGTTTCATCC CCACTGTGAG GGAAGTGCAG 2160
TGTCCAGAGG CCAATATTGA TACAGCCCTT TGTAAGGAAA GTCCGGGGCT CTGGGGAGCC 2220
AGCATCCTGA AGGCAGGTGC TGGGGTCCCT GGGGAGCAGC CTGTGGACCT TAACCTGCCT 2280
TTGGAAGCTC CCCCAATTTC AAAGGTCAGA GTGCATATTC AGGGTGCTCA GGTGAAAAGT 2340
CAAGAGGTCA CTATACACAG CATAGTGACA CCAGAGTTTG TAGATCTCTC AGTACCCAGG 2400
ACTTTTCCA CTCAGATTGT GCGGGAATCA GAGATCCCCA CGTCAGAGAT TCAAACACCT 2460
TCGTACGGAT TTTCCTTATT AAAAGTGAAA ATCCCAGAGC CCCACACGCA GGCTAGAGTG 2520
TACACAACAA TGACTCAACA CTCTAGGACT CAGGAGGGCA CAGAAGAGGC TCCCATACAA 2580
GCCACCCAG GAGTAGACTC CATTTCTGGA GATCTCCAGC CTGACACTGG AGAACCATT 2640
GAGATGATCT CTTCCAGCGT CAATGTACTG GGACAGCAAA CACTCACATT TGAAGTTCCT 2700

TCTGGCCACC AGCTTGCAGA CAGCTGTTCA GATGAGGAGC CAGCAGAAAT TCTTGAGTTT	2760
CCCCCTGATG ATAGCCAAGA GGCAACCACA CCACTGGCAG ATGAAGGCAG GGCTCCAAAA	2820
GACAAACCAG AAAGTAAAAA ATCTGGTCTG CTCTGGTTTTT GGCTTCCAAA CATTGGGTTT	2880
TCCTCTTCTG TTGATGAGAC AGGTGTTGAT TCCAAAAATG ACGTCCAGAG ATCTGCTCCC	2940
ATTCAAACAC AGCCTGAGGC ACGACCAGAG GCAGAACTGC CTAAAAAACA GGAGAAGGCA	3000
GGCTGGTTCC GATTTCCCAA ATTAGGGTTC TCCTCATCTC CTACCAAGAA AAGCAAAAGC	3060
ACCGAAGATG GGGCAGAGCT GGAAGAACAA AACTTCAAG AAGAAACAAT CACGTTTTTC	3120
GATGCCCCGAG AAAGTTTCTC CCCTGAAGAG AAGGAAGAGG GTGAACTGAT CGGGCCTGTG	3180
GGCACTGGGC TGGACTCCAG AGTGATGGTG ACATCCGCGG CAAGAACAGA GTTAATCCTG	3240
CCCGAGCAGG ACAGAAAAGC TGACGATGAA AGCAAAGGGT CAGGCCTGGG ACCAAATGAA	3300
GGCTGAGAGG TATGGCTCAT CGGTACAAGA GAGATGCAAA AAATAAGTT GGAAAGTAAA	3360
GGCTACACAC ACATATGGAG CACCCCATCC CACAGCACAT TACATCCACC TCACTTCACA	3420
GAACGGAGAA CAGAGCAGAA ATGACCAGAA CACCTTTGTC ACCATCACAC AGCCCTCCTA	3480
AAATGGAACC AAAGCTTCCC AGCTCCCTCA AAGCTTTGGA TGCAAAGAAG GCACCCTGAC	3540
TTCCACAAGA CACCAGAATT CACACGGTAC TCAGAGGCAC TGCTGGGGAA GTTTGTTGGT	3600
CTTTATTAGA TAAATTTCCTA GAGACCTGTC CATAATACCC AACAGAACAT GACTGTTTCT	3660
TTGAGGAAAAG GGTATAATG TCTGTGGTGT ACAAGTCGTT TTTGGTATAA CTTCTTTCCT	3720
GCTGCTGCTG CTTCCCGGCA AACATAGTTT TCCTATTTCA GGCAGAGTGC GGTATATTCC	3780
AGGAAACACT GTTTCCTACT CACTTAGCTT ACTTCTTTGT TGAATGCCTC ACTAATGGCA	3840
AGTTTCAAGA TGTTTTGGGT GACAATGCAC ACATGCTGGG CAAAAGGGTG ATGGCCAGTG	3900
GCTGGCAGCT GGGCCAGCAG AAGCTAGGAC ATCTGTGAGT TGTCATTCTC ATCTATCCAT	3960
GTCCACTGGC CTGCCAGCAT CCGCCAGTGC CTTGCCAGTG TGCACGGTCC CACACTGTGG	4020
CCCCTGAGTC CCCTAATGTA CACGCTGCAG CCAGAATGCA GATGGAGCTG GCTTGGCTGT	4080
TCCCTGGATG GGCAATAAAG AAAGTGCTGC ATCCCCAAAAA AAAAAAAAAA	4130

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met	Gln	Gln	Trp	Val	Pro	Gln	Ser	Cys	Xaa	Xaa	Leu	Ala	Leu	Gly	Glu	1	5	10	15
Arg	Val	Gln	Cys	Pro	Leu	Pro	Ser	Thr	Gln	Leu	Pro	Ser	Pro	Gly	Thr	20	25	30	
Cys	Val	Ser	Gln	Gly	Pro	Glu	Glu	Leu	Val	Ala	Ser	Leu	Gln	Thr	Ser	35	40	45	
Val	Val	Ala	Xaa	Gly	Glu	Ala	Pro	Ser	Glu	Asp	Ala	Asp	His	Glu	Gly	50	55	60	
Lys	Gly	Ser	Pro	Leu	Lys	Met	Pro	Lys	Ile	Lys	Leu	Pro	Ser	Phe	Arg	65	70	75	80
Trp	Ser	Pro	Lys	Lys	Glu	Thr	Gly	Pro	Lys	Val	Asp	Pro	Glu	Cys	Ser	85	90	95	
Val	Glu	Asp	Ser	Lys	Leu	Ser	Leu	Val	Leu	Asp	Lys	Asp	Glu	Val	Ala	100	105	110	
Pro	Gln	Ser	Ala	Ile	His	Met	Asp	Leu	Pro	Pro	Glu	Arg	Asp	Gly	Glu	115	120	125	
Lys	Gly	Arg	Ser	Thr	Lys	Pro	Gly	Phe	Ala	Met	Pro	Lys	Leu	Ala	Leu	130	135	140	
Pro	Lys	Met	Lys	Ala	Ser	Lys	Ser	Gly	Val	Ser	Leu	Pro	Gln	Arg	Asp	145	150	155	160
Val	Asp	Pro	Ser	Leu	Ser	Ser	Ala	Thr	Ala	Gly	Gly	Ser	Phe	Gln	Asp	165	170	175	
Thr	Glu	Lys	Ala	Ser	Ser	Asp	Gly	Gly	Arg	Gly	Gly	Leu	Gly	Ala	Thr	180	185	190	
Ala	Ser	Ala	Thr	Gly	Ser	Glu	Gly	Val	Asn	Leu	His	Arg	Pro	Gln	Val	195	200	205	
His	Ile	Pro	Ser	Leu	Gly	Phe	Ala	Lys	Pro	Asp	Leu	Arg	Ser	Ser	Lys	210	215	220	
Ala	Lys	Val	Glu	Val	Ser	Gln	Pro	Glu	Ala	Asp	Leu	Pro	Leu	Pro	Lys	225	230	235	240
His	Asp	Leu	Ser	Thr	Glu	Gly	Asp	Ser	Arg	Gly	Cys	Gly	Leu	Glu	Asp	245	250	255	
Val	Pro	Val	Ser	Gln	Pro	Cys	Gly	Glu	Gly	Ile	Ala	Pro	Thr	Pro	Glu	260	265	270	

Asp Pro Leu Gln Pro Ser Cys Arg Lys Pro Asp Ala Glu Val Leu Thr
 275 280 285
 Val Glu Ser Pro Glu Glu Glu Ala Met Thr Lys Asp Ser Gln Glu Ser
 290 295 300
 Trp Phe Lys Met Pro Lys Phe Arg Met Pro Ser Leu Arg Arg Ser Phe
 305 310 315 320
 Arg Asp Arg Gly Gly Ala Gly Lys Leu Glu Val Ala Gln Thr Gln Ala
 325 330 335
 Pro Ala Ala Thr Gly Gly Glu Ala Ala Ala Lys Val Lys Glu Phe Leu
 340 345 350
 Val Ser Gly Ser Asn Val Glu Ala Ala Met Ser Leu Gln Leu Pro Glu
 355 360 365
 Ala Asp Ala Glu Val Thr Ala Ser Glu Ser Lys Ser Ser Thr Asp Ile
 370 375 380
 Leu Arg Cys Asp Leu Asp Ser Thr Gly Leu Lys Leu His Leu Ser Thr
 385 390 395 400
 Ala Gly Met Thr Gly Asp Glu Leu Ser Thr Ser Glu Val Arg Ile His
 405 410 415
 Pro Ser Lys Gly Pro Leu Pro Phe Gln Met Pro Gly Met Arg Leu Pro
 420 425 430
 Glu Thr Gln Val Leu Pro Gly Glu Ile Asp Glu Thr Pro Leu Ser Lys
 435 440 445
 Pro Gly His Asp Leu Ala Ser Met Glu Asp Lys Thr Glu Lys Trp Ser
 450 455 460
 Ser Gln Pro Glu Gly Pro Leu Lys Leu Lys Ala Ser Ser Thr Asp Met
 465 470 475 480
 Pro Ser Gln Ile Ser Val Val Asn Val Asp Gln Leu Trp Glu Asp Ser
 485 490 495
 Val Leu Thr Val Lys Phe Pro Lys Leu Met Val Pro Arg Phe Ser Phe
 500 505 510
 Ala Ala Pro Ser Ser Glu Asp Asp Val Phe Ile Pro Thr Val Arg Glu
 515 520 525
 Val Gln Cys Pro Glu Ala Asn Ile Asp Thr Ala Leu Cys Lys Glu Ser
 530 535 540
 Pro Gly Leu Trp Gly Ala Ser Ile Leu Lys Ala Gly Ala Gly Val Pro
 545 550 555 560
 Gly Glu Gln Pro Val Asp Leu Asn Leu Pro Leu Glu Ala Pro Pro Ile
 565 570 575

Ser Lys Val Arg Val His Ile Gln Gly Ala Gln Val Glu Ser Gln Glu
580 585 590

Val Thr Ile His Ser Ile Val Thr Pro Glu Phe Val Asp Leu Ser Val
595 600 605

Pro Arg Thr Phe Ser Thr Gln Ile Val Arg Glu Ser Glu Ile Pro Thr
610 615 620

Ser Glu Ile Gln Thr Pro Ser Tyr Gly Phe Ser Leu Leu Lys Val Lys
625 630 635 640

Ile Pro Glu Pro His Thr Gln Ala Arg Val Tyr Thr Thr Met Thr Gln
645 650 655

His Ser Arg Thr Gln Glu Gly Thr Glu Glu Ala Pro Ile Gln Ala Thr
660 665 670

Pro Gly Val Asp Ser Ile Ser Gly Asp Leu Gln Pro Asp Thr Gly Glu
675 680 685

Pro Phe Glu Met Ile Ser Ser Ser Val Asn Val Leu Gly Gln Gln Thr
690 695 700

Leu Thr Phe Glu Val Pro Ser Gly His Gln Leu Ala Asp Ser Cys Ser
705 710 715 720

Asp Glu Glu Pro Ala Glu Ile Leu Glu Phe Pro Pro Asp Asp Ser Gln
725 730 735

Glu Ala Thr Thr Pro Leu Ala Asp Glu Gly Arg Ala Pro Lys Asp Lys
740 745 750

Pro Glu Ser Lys Lys Ser Gly Leu Leu Trp Phe Trp Leu Pro Asn Ile
755 760 765

Gly Phe Ser Ser Ser Val Asp Glu Thr Gly Val Asp Ser Lys Asn Asp
770 775 780

Val Gln Arg Ser Ala Pro Ile Gln Thr Gln Pro Glu Ala Arg Pro Glu
785 790 795 800

Ala Glu Leu Pro Lys Lys Gln Glu Lys Ala Gly Trp Phe Arg Phe Pro
805 810 815

Lys Leu Gly Phe Ser Ser Ser Pro Thr Lys Lys Ser Lys Ser Thr Glu
820 825 830

Asp Gly Ala Glu Leu Glu Glu Gln Lys Leu Gln Glu Glu Thr Ile Thr
835 840 845

Phe Phe Asp Ala Arg Glu Ser Phe Ser Pro Glu Glu Lys Glu Glu Gly
850 855 860

Glu Leu Ile Gly Pro Val Gly Thr Gly Leu Asp Ser Arg Val Met Val
865 870 875 880

Thr Ser Ala Ala Arg Thr Glu Leu Ile Leu Pro Glu Gln Asp Arg Lys
885 890 895

Ala Asp Asp Glu Ser Lys Gly Ser Gly Leu Gly Pro Asn Glu Gly
900 905 910

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCTCGTCTCG	CCGGGCTGTT	CGCGGGCAGG	CCCTGCCCTG	AAGGGACGAA	TCGGCTTGGA	60
GCGCGGGAGG	TGGAGTCGGC	CCCGGCGGTC	GCTCCCTGGA	CCCAACCCGA	GGCTGACCCA	120
KGCCCCTGCC	CATGCGGGGC	GCCCCCTGGCT	CGGAAGAGTC	CCCCGGGCGG	GGAGCAGCTC	180
CAGGCAGCGG	CCCCGGAGGA	AGAGGAAGAA	GGGACAGTGC	TCAGCTTGGG	GGACCCGGAC	240
CCTCGCCGCG	GCATTTGGAG	CCGGGGGCAG	TCCCGAACTC	TGTGCTTGGC	ACCGCCGCTC	300
CGAGTAGGGC	AGCGCCTGCC	GGGACTCTGA	CCCGGACCCC	CTGCGCCTCG	TAGGCGGCGG	360
CGCCGCCGCG	CCACCCTGTT	CTTCCGTGTC	TCCCTCTGCC	TGGCGGCAGT	CACGGCCAAG	420
AGAGTATTAT	GAGGGAGGCC	GAGGACTTCA	TGCTCCGGAC	AGAGAAACGG	CGCTGGGATT	480
AGGGATTGCC	ACTTCTGAGA	GGATGCTGGG	AATCTGCAGG	GGGAGACGGA	AATTCTTGGC	540
TGCCTCGTTG	AGTCTTCTCT	GCATCCCAGC	CATCACCTGG	ATTTACCTGT	TTTCTGGGAG	600
CTTCGAAGAT	GGAAAGCCCG	TGTCTCTGTC	ACCGCTGGAG	TCCCAGGCAC	ACAGCCCCAG	660
GTACACGGCC	TCCAGCCAGC	GGGAGCGCGA	GAGCCTGGAG	GTGCGCATGC	GCGAGGTGGA	720
GGAGGAGAAC	CGCGCCCTCC	GCAGGCAGCT	CAGCCTGGCC	CAGGGCCGAG	CCCCATCCCA	780
TCGCCGAGGC	AACCACTCCA	AGACCTACTC	CATGGAGGAG	GGCACTGGAG	ACAGCGAGAA	840
CCTTCGGGCT	GGCATCGTGG	CAGGCAACAG	CTCCGAGTGT	GGGCAGCAGC	CGGTCTGTGA	900
GAAATGCGAG	ACAATCCACG	TTGCTATTGT	CTGCGCCGGA	TACAATGCCA	GCCGGGATGT	960
CGTCACCCTG	GTCAAATCCG	TCCTGTTCCA	TAGACGGAAC	CCTCTGCACT	TCCACCTTAT	1020
TGCTGACTCC	ATTGCGGAGC	AGATCCTGGC	CACGCTCTTC	CAGACCTGGA	TGGTGCCCGC	1080

TGTGCGTGTG	GACTTCTACA	ATGCAGACGA	GCTCAAGTCT	GAAGTTTCCT	GGATCCCCAA	1140
TAAACATTAC	TCTGGGATTT	ATGGTCTGAT	GAAGCTTGTC	CTGACCAAGA	CTCTTCCTGC	1200
CAACCTGGAG	AGAGTCATCG	TCCTTGACAC	GGATATCACC	TTTGCCACTG	ACATTGCAGA	1260
GCTGTGGGCT	GTGTTCCACA	AGTTCAAAGG	TCAGCAAGTC	CTGGGCTTGG	TGGAGAACCA	1320
GAGTGACTGG	TACCTTGGA	ACCTGTGGAA	AAATCACCGC	CCATGGCCAG	CCCTTGGAAG	1380
AGGCTACAAC	ACAGGGGTGA	TCCTGTTACT	TCTGGATAAG	CTGCGGAAGA	TGAAATGGGA	1440
GCAGATGTGG	AGGCTGACCG	CAGAGAGGGA	GCTCATGGGC	ATGCTCTCTA	CATCCTTAGC	1500
TGACCAGGAT	ATTTTCAATG	CCGTCATCAA	ACAAAACCCC	TTCCTTGTGT	ACCAGCTCCC	1560
CTGCTTCTGG	AATGTGCAGC	TGTCAGACCA	CACCCGCTCC	GAGCAGTGCT	ACAGAGACGT	1620
GTCTGATCTA	AAGGTCATTC	ACTGGAACTC	CCCCAAGAAG	CTCCGGGTGA	AGAACAAGCA	1680
TGTGGAGTTT	TTTCGCAACC	TCTACCTGAC	CTTCCTGGAG	TATGACGGCA	ATCTTCTGAG	1740
GCGGGAAC TG	TTTGGCTGCC	CCAGTGAGGC	TGATGTCAAC	AGTGAAAACC	TCCAGAAGCA	1800
GCTGTCTGAG	CTGGACGAGG	ACGACCTGTG	CTATGAGTTC	CGGCGAGAGC	GCTTCACTGT	1860
CCACCGCACC	CACCTGTACT	TCCTGCACTA	CGAGTATGAG	CCTGCAGCAG	ACAGCACGGA	1920
CGTCACCTTG	GTGCTCAGC	TGTCCATGGA	CAGGCTCCAG	ATGCTGGAGG	CCATCTGCAA	1980
GCACTGGGAG	GGGCCCATCA	GCCTGGCCCT	CTACCTGTCA	GACGCCGAGG	CCCAGCAGTT	2040
CCTCCGCTAC	GCACAGGGCT	CTGAGGTGCT	TATGAGCCGC	CACAACGTGG	GCTACCACAT	2100
CGTGTAACAAG	GAGGGCCAGT	TCTACCCCGT	GAACCTGCTG	CGCAACGTGG	CCATGAAGCA	2160
CATCAGCACT	CCCTACATGT	TCCTGTCTGA	CATTGACTTC	CTGCCCATGT	ATGGGCTCTA	2220
TGAGTACCTC	AGGAAGTCTG	TCATCCAGCT	CGATCTTGCC	AACACCAAGA	AAGCAATGAT	2280
TGTCCCCGCG	TTGAGACAC	TGCGCTACCG	GCTGTCCCTC	CCCAAGTCAA	AAGCGGAGTT	2340
GCTGTCAATG	CTGGACATGG	GGACCTCTT	CACATTGAGG	TACCACGTCT	GGACGAAAGG	2400
CCACGCACCC	ACAACTTCG	CCAAGTGGCG	GACCGCCACC	ACGCCTTACC	GGGTTGAGTG	2460
GGAGGCCGAT	TTTGAGCCGT	ATGTTGTTGT	GAGACGTGAC	TGCCCCGAGT	ACGACCGGAG	2520
GTTTGTAGGC	TTTGGCTGGA	ACAAAGTGGC	TCATATCATG	GAGCTGGATG	TGCAGGAGTA	2580
TGAGTTCATT	GTGCTGCCCA	ACGCCTACAT	GATCCACATG	CCTCATGCCC	CCAGCTTCGA	2640
CATTACCAAG	TTCCGTTCGA	ACAAGCAATA	CCGCATCTGT	CTCAAAACCC	TCAAGGAAGA	2700
GTTTCAGCAG	GACATGTCCC	GCCGCTACGG	CTTTGCTGCC	CTGAAATATC	TCACAGCCGA	2760
GAACAACAGC	TAGCACCAAG	AAGCCCACCA	CTAGGGGGAG	ACATGCTGTA	GGGGAAGTGC	2820

CACTCGCTGT TTGGGGCCCG GCCTTCAAAT TCAAAATTGA GCCATGCTTT TTCGGTTTGT	2880
TTTTATTTAT CTCTTTGGCC CAGCCAAGCT GCCCTCACTA CAGAGACCTT GGACAAGGAT	2940
CCAGCCAGTC CCTCTCTGCC CCACAACCCT GCATTCCCAG AGGTTAGCTA TGCAGCCCAC	3000
CTAGATGAGT CTCTTCAAGA ATGGGAAATC AAGGGGTGAC AGGGAGTAAA AGGGTTATCA	3060
TCTTACTGCA AAGCCACAAG ATCAGGGCAG GGCTTTAGGA TGTTCCTGGAT GCTTTTTAAT	3120
AATTATGCTT CCCATCATAA CTGGGGAGAA AGGGAAGTCA GGGTCTAGG GGTATTTCGT	3180
CCCAGGAAAT AGAAGTGAAA TTGTCTTTAT TAAGTGAAAA CTTTCCCCTT TGCCCTGCAA	3240
TGTAGCTGGG CATTCAAACG GAGGGCAAAC CGATGATCTA AACCAACCAC TTGGAAAAAC	3300
CCAATGGGGA CATTGTAACC AGAGGGTCCT GGAGGTGGGG TTGATGGGTT TCCTTATCCC	3360
CAAAGTCACT CCTGTTTTGT TTTGTTTTTC TTTGGGGGTT TTGTTTATTT TTGGGGCTGG	3420
CAATCCAAAA TAGAAAACTT GATCCTTTGA GGCTCTAAAG GAAAATCAGC TGCCTCTACC	3480
AACCACCTC TATCAGCAGT GGCCAGGAA GGAGGTCAAG CATCTTCGGC CGATATTTAA	3540
ACATGGGCAG CTTCTTCAG GATGATCACC GAGGCTCCCG TGACTTTGAA CTCCTACTC	3600
TCCAGAATCC AGGGGCTATA GCGATGGGGA CTGCGGAATT ACGAGGGCTG GCTGTTTTAC	3660
ACCGGTCACA TTTTCTATTG GCAGTGACTG ATTCATGGGA AAGGGCTTTG AAGGAACTAC	3720
TTCAGTGCAC ACACAAGGTA CGAACCTYTC AGGCCTTTCG AAGAACTTTC ATAATTCATG	3780
AAAGCCCAGT TYTGAAGATT CACGTATCCA TYTGAGACC TACAGGAAGA AAGTGATTGG	3840
GTTCTCTGG TTCTTGCCCTG CTTCACTGTG GATGGGAAGA GGTGACAACC TCAGTCTCCC	3900
TTTGGGACCT GTCCAAGGGT AGGCAACCAC CTTACCTTC ACACAGATTG AGGAGACACT	3960
GGACTTTTTTA CCCATTTTCT TTAATYTTCA ATATTAATAT TGTGTTTACA TTGATGAGAA	4020
CAAGAGTTAA TGCCCTACCC TCTGCTGGGC TGTGTGTATT GAGTTGCAAT GTGACCAGCG	4080
AAAGCTGCAT TTAATAAATG AAAGTACAGA CTGAAAAAAA AAAAAAAAAA AAAAAAAAAA	4140
AA	4142

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met	Leu	Gly	Ile	Cys	Arg	Gly	Arg	Arg	Lys	Phe	Leu	Ala	Ala	Ser	Leu	1	5	10	15
Ser	Leu	Leu	Cys	Ile	Pro	Ala	Ile	Thr	Trp	Ile	Tyr	Leu	Phe	Ser	Gly	20	25	30	
Ser	Phe	Glu	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	Pro	Leu	Glu	Ser	Gln	35	40	45	
Ala	His	Ser	Pro	Arg	Tyr	Thr	Ala	Ser	Ser	Gln	Arg	Glu	Arg	Glu	Ser	50	55	60	
Leu	Glu	Val	Arg	Met	Arg	Glu	Val	Glu	Glu	Glu	Asn	Arg	Ala	Leu	Arg	65	70	75	80
Arg	Gln	Leu	Ser	Leu	Ala	Gln	Gly	Arg	Ala	Pro	Ser	His	Arg	Arg	Gly	85	90	95	
Asn	His	Ser	Lys	Thr	Tyr	Ser	Met	Glu	Glu	Gly	Thr	Gly	Asp	Ser	Glu	100	105	110	
Asn	Leu	Arg	Ala	Gly	Ile	Val	Ala	Gly	Asn	Ser	Ser	Glu	Cys	Gly	Gln	115	120	125	
Gln	Pro	Val	Val	Glu	Lys	Cys	Glu	Thr	Ile	His	Val	Ala	Ile	Val	Cys	130	135	140	
Ala	Gly	Tyr	Asn	Ala	Ser	Arg	Asp	Val	Val	Thr	Leu	Val	Lys	Ser	Val	145	150	155	160
Leu	Phe	His	Arg	Arg	Asn	Pro	Leu	His	Phe	His	Leu	Ile	Ala	Asp	Ser	165	170	175	
Ile	Ala	Glu	Gln	Ile	Leu	Ala	Thr	Leu	Phe	Gln	Thr	Trp	Met	Val	Pro	180	185	190	
Ala	Val	Arg	Val	Asp	Phe	Tyr	Asn	Ala	Asp	Glu	Leu	Lys	Ser	Glu	Val	195	200	205	
Ser	Trp	Ile	Pro	Asn	Lys	His	Tyr	Ser	Gly	Ile	Tyr	Gly	Leu	Met	Lys	210	215	220	
Leu	Val	Leu	Thr	Lys	Thr	Leu	Pro	Ala	Asn	Leu	Glu	Arg	Val	Ile	Val	225	230	235	240
Leu	Asp	Thr	Asp	Ile	Thr	Phe	Ala	Thr	Asp	Ile	Ala	Glu	Leu	Trp	Ala	245	250	255	
Val	Phe	His	Lys	Phe	Lys	Gly	Gln	Gln	Val	Leu	Gly	Leu	Val	Glu	Asn	260	265	270	
Gln	Ser	Asp	Trp	Tyr	Leu	Gly	Asn	Leu	Trp	Lys	Asn	His	Arg	Pro	Trp				

275	280	285
Pro Ala Leu Gly Arg Gly Tyr Asn Thr Gly Val Ile Leu Leu Leu Leu 290	295	300
Asp Lys Leu Arg Lys Met Lys Trp Glu Gln Met Trp Arg Leu Thr Ala 305	310	315 320
Glu Arg Glu Leu Met Gly Met Leu Ser Thr Ser Leu Ala Asp Gln Asp 325	330	335
Ile Phe Asn Ala Val Ile Lys Gln Asn Pro Phe Leu Val Tyr Gln Leu 340	345	350
Pro Cys Phe Trp Asn Val Gln Leu Ser Asp His Thr Arg Ser Glu Gln 355	360	365
Cys Tyr Arg Asp Val Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro 370	375	380
Lys Lys Leu Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Leu 385	390	395 400
Tyr Leu Thr Phe Leu Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu 405	410	415
Phe Gly Cys Pro Ser Glu Ala Asp Val Asn Ser Glu Asn Leu Gln Lys 420	425	430
Gln Leu Ser Glu Leu Asp Glu Asp Asp Leu Cys Tyr Glu Phe Arg Arg 435	440	445
Glu Arg Phe Thr Val His Arg Thr His Leu Tyr Phe Leu His Tyr Glu 450	455	460
Tyr Glu Pro Ala Ala Asp Ser Thr Asp Val Thr Leu Val Ala Gln Leu 465	470	475 480
Ser Met Asp Arg Leu Gln Met Leu Glu Ala Ile Cys Lys His Trp Glu 485	490	495
Gly Pro Ile Ser Leu Ala Leu Tyr Leu Ser Asp Ala Glu Ala Gln Gln 500	505	510
Phe Leu Arg Tyr Ala Gln Gly Ser Glu Val Leu Met Ser Arg His Asn 515	520	525
Val Gly Tyr His Ile Val Tyr Lys Glu Gly Gln Phe Tyr Pro Val Asn 530	535	540
Leu Leu Arg Asn Val Ala Met Lys His Ile Ser Thr Pro Tyr Met Phe 545	550	555 560
Leu Ser Asp Ile Asp Phe Leu Pro Met Tyr Gly Leu Tyr Glu Tyr Leu 565	570	575
Arg Lys Ser Val Ile Gln Leu Asp Leu Ala Asn Thr Lys Lys Ala Met		

580	585	590
Ile Val Pro Ala Phe Glu Thr	Leu Arg Tyr Arg Leu Ser Phe Pro Lys	
595	600	605
Ser Lys Ala Glu Leu Leu Ser Met Leu Asp Met Gly Thr Leu Phe Thr		
610	615	620
Phe Arg Tyr His Val Trp Thr Lys Gly His Ala Pro Thr Asn Phe Ala		
625	630	635
Lys Trp Arg Thr Ala Thr Thr Pro Tyr Arg Val Glu Trp Glu Ala Asp		
645	650	655
Phe Glu Pro Tyr Val Val Val Arg Arg Asp Cys Pro Glu Tyr Asp Arg		
660	665	670
Arg Phe Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Met Glu Leu		
675	680	685
Asp Val Gln Glu Tyr Glu Phe Ile Val Leu Pro Asn Ala Tyr Met Ile		
690	695	700
His Met Pro His Ala Pro Ser Phe Asp Ile Thr Lys Phe Arg Ser Asn		
705	710	715
Lys Gln Tyr Arg Ile Cys Leu Lys Thr Leu Lys Glu Glu Phe Gln Gln		
725	730	735
Asp Met Ser Arg Arg Tyr Gly Phe Ala Ala Leu Lys Tyr Leu Thr Ala		
740	745	750
Glu Asn Asn Ser		
755		

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGCACCGGTG GTCGGCTGTT GGGTGTGGAG TTTCCAGCG CCCCTCGGGT CCGACCCCTTT	60
GAGCGTTCTG CTCCGGCGCC AGCCTACCTC GCTCCTCGGC GCCATGACCA CAACCACCAC	120
CTTCAAGGGA GTCGACCCCA ACAGCAGGAA TAGCTCCCGA GTTTTGCGGC CTCCAGGTGG	180
TGGATCCAAT TTTTCATTAG GTTTTGATGA ACCAACAGAA CAACCTGTGA GGAAGAACAA	240

AATGGCCTCT AATATCTTTG GGACACCTGA AGAAAATCAA GCTTCTTGGG CCAAGTCAGC 300
 AGGTGCCAAG TCTAGTGGTG GCAGGGAAGA CTTGGAGTCA TCTGGACTGC AGAGAAGGAA 360
 CTCCTCTGAA GCAAGCTCCG GAGACTTCTT AGATCTGAAG GGAGAAGGTG ATATTCATGA 420
 AAATGTGGAC ACAGACTTGC CAGGCAGCCT GGGGCAGAGT GAAGAGAAGC CCGTGCCTGC 480
 TGC GCCTGTG CCCAGCCCGG TGGCCCCGGC CCCAGTGCCA TCCAGAAGAA ATCCCCCTGG 540
 CGGCAAGTCC AGCCTCGTCT TGGGTTAGCT CTGACTGTCC TGAACGCTGT CGTTCTGTCT 600
 GTTTCCTCCA TGCTTGTGAA CTGCACAACT TGAGCCTGAC TGTACATCTC TTGGATTTGT 660
 TTCATTAAAA AGAAGCACTT TATGTACTGC TGTCTTTTTT TTTTTTCTT TTGAAGAACA 720
 GGTTCCTCTC TGTCCTTGAC TCTTGGGTCT GTGGGCCATG GCATGAGTGT TTTCTAGTAG 780
 TAGATTGGAG GGAAAGCTTT GTGACACTTA GTACTGTGTT TTTAAGAAGA AATAATTTGG 840
 TTCCAGATGT GTTAGAGGAT CTTTTGTACT GAGGTTTTTA ACACTTTACT TGGGTTTACC 900
 AAGCCTCAAC TGGACAGACC ATAAACAGTC CACAGGCACC GTTCCTGCCA GGCCCCAACC 960
 CACAGGGAGT CTCTCCGCAG AGCCTTCTTG GTGTTGCCCT AACTTGCCAG TGGCCTTTGC 1020
 TCAGAGCCTC CTCCTGTGAC ATGTGAACAA TGAAGAGGCC TGCGCYTCCT GCCTTGCCGC 1080
 CTGCAAAGCA AAGAACTGC CTTTTATTTT TTAACCTTAA AAAGTAGCCA GATAGTAACA 1140
 AGACTGGCTG GCTGATGAGC AAAGCYTTTG CTCTCACGCA GAGGAAGGCT TGGATGTACA 1200
 ATGAAACTGC CTGGAATAA AAGCAGTGAA GCAAGGGAGG CAATCACACT GAAGCGGGTC 1260
 TTCCTCCAGG AACGGGGTCC CACAGGCGTG TTGTTTTAAA TAACCTGATG CTGTGTGCAT 1320
 GATGCTGGTG CTTGACCATG AAAGGAAAGT CTCATCCTTA AAATGTGTTG TACTTCACAA 1380
 TCCTGGACTG TTGCTTCAAG TAAACAATAT CCACATTTTG AAAAAAAAAA AAAAA 1435

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Met Thr Thr Thr Thr Thr Phe Lys Gly Val Asp Pro Asn Ser Arg Asn

1	5	10	15
Ser Ser Arg Val Leu Arg Pro Pro Gly Gly Gly Ser Asn Phe Ser Leu			
20	25	30	
Gly Phe Asp Glu Pro Thr Glu Gln Pro Val Arg Lys Asn Lys Met Ala			
35	40	45	
Ser Asn Ile Phe Gly Thr Pro Glu Glu Asn Gln Ala Ser Trp Ala Lys			
50	55	60	
Ser Ala Gly Ala Lys Ser Ser Gly Gly Arg Glu Asp Leu Glu Ser Ser			
65	70	75	80
Gly Leu Gln Arg Arg Asn Ser Ser Glu Ala Ser Ser Gly Asp Phe Leu			
85	90	95	
Asp Leu Lys Gly Glu Gly Asp Ile His Glu Asn Val Asp Thr Asp Leu			
100	105	110	
Pro Gly Ser Leu Gly Gln Ser Glu Glu Lys Pro Val Pro Ala Ala Pro			
115	120	125	
Val Pro Ser Pro Val Ala Pro Ala Pro Val Pro Ser Arg Arg Asn Pro			
130	135	140	
Pro Gly Gly Lys Ser Ser Leu Val Leu Gly			
145	150		

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1904 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CAGCGTCGCG CGCGCTACCA CACCCAGGTT CGGCCCGTAG GCGTCTGGCA GCCC GGCGCC	60
ATCTTCATCG AGCGCCATGG CCGCAGCCTG CGGGCCGGGA GCGGCCGGGT ACTGCTTGCT	120
CCTCGGCTTG CATTTGTTTC TGCTGACCGC GGGCCCTGCC CTGGGCTGGA ACGACCCTGA	180
CAGAATGTTG CTGCGGGATG TAAAAGCTCT TACCCTCCAC TATGACCGCT ATACCACCTC	240
CCGCAGGCTG GATCCCATCC CACAGTTGAA ATGTGTTGGA GGCACAGCTG GTTGTGATTC	300
TTATACCCCA AAAGTCATAC AGTGTCAGAA CAAAGGCTGG GATGGGTATG ATGTACAGTG	360
GGAATGTAAG ACGGACTTAG ATATTGCATA CAAATTTGGA AAAACTGTGG TGAGCTGTGA	420

AGGCTATGAG TCCTCTGAAG ACCAGTATGT ACTAAGAGGT TCTTGTGGCT TGGAGTATAA 480
TTTAGATTAT ACAGAACTTG GCCTGCAGAA ACTGAAGGAG TCTGGAAAGC AGCACGGCTT 540
TGCCTCTTTC TCTGATTATT ATTATAAGTG GTCCTCGGCG GATTCCTGTA ACATGAGTGG 600
ATTGATTACC ATCGTGGTAC TCCTTGGGAT CGCCTTTGTA GTCTATAAGC TGTTCCTGAG 660
TGACGGGCAG TATTCTCCTC CACCGTACTC TGAGTATCCT CCATTTTCCC ACCGTTACCA 720
GAGATTCACC AACTCAGCAG GACCTCCTCC CCCAGGCTTT AAGTCTGAGT TCACAGGACC 780
ACAGAATACT GGCCATGGTG CAACTTCTGG TTTTGGCAGT GCTTTTACAG GACAACAAGG 840
ATATGAAAAT TCAGGACCAG GGTTCCTGGAC AGGCTTGGGA ACTGGTGGAA TACTAGGATA 900
TTTGTTTGGC AGCAATAGAG CGGCAACACC CTTCTCAGAC TCGTGGTACT ACCCGTCTTA 960
TCCTCCCTCC TACCCTGGCA CGTGGAATAG GGCTTACTCA CCCCTTCATG GAGGCTCGGG 1020
CAGCTATTCG GTATGTTCAA ACTCAGACAC GAAAACCAGA ACTGCATCAG GATATGGTGG 1080
TACCAGGAGA CGATAAAGTA GAAAGTTGGA GTCAAACACT GGATGCAGAA ATTTTGGATT 1140
TTTCATCACT TTCTCTTTAG AAAAAAAGTA CTACCTGTTA ACAATTGGGA AAAGGGGATA 1200
TTCAAAAGTT CTGTGGTGTT ATGTCCAGTG TAGCTTTTTG TATTCTATTA TTTGAGGCTA 1260
AAAGTTGATG TGTGACAAAA TACTTATGTG TTGTATGTCA GTGTAACATG CAGATGTATA 1320
TTGCAGTTTT KGAAAGTGAT CATTACTGTG GAATGCTAAA AATACATTAA TTTCTAAAC 1380
CTGTGATGCC CTAAGAAGCA TTAAGAATGA AGGTGTTGTA CTAATAGAAA CTAAGTACAG 1440
AAAATTTTCTAG TTTTAGGTGG TTGTAGCTGA TGAGTTATTA CCTCATAGAG ACTATAATAT 1500
TCTATTTGGT ATTATATTAT TTGATGTTTG CTGTTCTTCA AACATTTAAA TCAAGCTTTG 1560
GACTAATTAT GCTAATTTGT GAGTTCTGAT CACTTTTGAG CTCTGAAGCT TTGAATCATT 1620
CAGTGGTGGA GATGGCCTTC TGGTAACTGA ATATTACCTT CTGTAGGAAA AGGTGGAAAA 1680
TAAGCATCTA GAAGGTTGTT GTGAATGACT CTGTGCTGGC AAAAATGCTT GAAACCTCTA 1740
TATTTCTTTC GTTCATAAGA GGTAAAGGTC AAATTTTTC ACAAAGTCT TTTAATAACA 1800
AAAGCATGCA GTTCTCTGTG AAATCTCAAA TATTGTTGTA ATAGTCTGTT TCAATCTTAA 1860
AAAGAATCAA TAAAAACAAA CAAGGAAAAA AAAAAAAAAA AAAA 1904

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu
 1             5             10             15

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn
 20             25             30
Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
 35             40             45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
 50             55             60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
 65             70             75             80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
 85             90             95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
100             105             110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
115             120             125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
130             135             140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145             150             155             160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
165             170             175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
180             185             190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
195             200             205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
210             215             220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225             230             235             240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
245             250             255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile

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260	265	270
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp		
275	280	285
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn		
290	295	300
Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys		
305	310	315
Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr		
325	330	335
Arg Arg Arg		

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CTGTCTGGCG GCGGCAGCAT GCGGCGGGG GCGGCTGAGG CAGCTGTAGC GGCCGTGGAG	60
GAGGTCGGCT CAGCCGGGCA GTTTGAGGAG CTGCTGCGCC TCAAAGCCAA GTCCCTCCTT	120
GTGGTCCATT TCTGGGCACC ATGGGCTCCA CAGTGTGCAC AGATGAACGA AGTTATGGCA	180
GAGTTAGCTA AAGAACTCCC TCAAGTTTCA TTTGTGAAGT TGGAAGCTGA AGGTGTTCTT	240
GAAGTATCTG AAAAATATGA AATTAGCTCT GTTCCCACTT TTCTGTTTTT CAAGAATTCT	300
CAGAAAATCG ACCGATTAGA TGGTGCACAT GCCCCAGAGT TGACCAAAAA AGTTCAGCGA	360
CATGCATCTA GTGGCTCCTT CCTACCCAGC GCTAATGAAC ATCTTAAAGA AGACCTCAGC	420
CTTCGCCTGA AAAAGCTGAC TCACGCTGCC CCCTGCATGC TGTTTCATGAA GGGAACACCT	480
CAAGAACCAC GCTGTGGTTT CAGCAAGCAG ATGGTGGAAA TCCTTCACAA ACACAATATT	540
CAGTTCAGCA GCTTTGATAT CTTCTCAGAT GAAGAAGTTC GACAGGGGCT CAAAACGTAC	600
TCTAATTGGC CCACCTATCC TCAGCTCTAT GTTTCTGGAG AGCTAATAGG AGGACTTGAC	660
ATAATTAAGG AGCTGGAAGC ATCAGAAGAG CTGGACACGA TCTGTCCCAA AGCTCCCCAA	720
TTAGAGGAAA GGCTCAAAGT GCTGACAAAT AAAGCTTCTG TGATGCTCTT TATGAAAGGA	780

AACAAACAGG AAGCAAAATG TGGATTCAGC AAACAAATTC TGGAAATACT AAATAGTACT 840
GGTGTGTAAT ATGAAACATT CGATATATTG GAGGATGAAG AAGTTCGGCA AGGATTAAAA 900
GCTTACTCAA ATTGGCCAAC ATACCCTCAG CTGTATGTGA AAGGGGAGCT GGTGGGAGGA 960
TTGGATATTG TGAAGGAACT GAAAGAAAAT GGTGAATTGC TGCCTATACT GAGAGGAGAA 1020
AATTAATAAA TCTTAAACTT GGTGCCCAAC TATTGTAAGA AATATTTAAT TACATTGGGA 1080
GCAGTTCATG ATTTAGTCCT CAGAAATGGA CTAGGAATAG AAAATTCCTG CTTTCTCAGT 1140
TACATGTTTT GTGTATTTCA CAATGTCGTG CTAAATAAAT GTATGTTACA TTTTTTTCCC 1200
ACCAAAAATA GAATGCAATA AACATCTTCA AATTATTAAC AATAAAAAAA AAAAAAAAAA 1260

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Ala Ala Gly Ala Ala Glu Ala Ala Val Ala Ala Val Glu Glu Val
1 5 10 15
Gly Ser Ala Gly Gln Phe Glu Glu Leu Leu Arg Leu Lys Ala Lys Ser
20 25 30
Leu Leu Val Val His Phe Trp Ala Pro Trp Ala Pro Gln Cys Ala Gln
35 40 45
Met Asn Glu Val Met Ala Glu Leu Ala Lys Glu Leu Pro Gln Val Ser
50 55 60
Phe Val Lys Leu Glu Ala Glu Gly Val Pro Glu Val Ser Glu Lys Tyr
65 70 75 80
Glu Ile Ser Ser Val Pro Thr Phe Leu Phe Phe Lys Asn Ser Gln Lys
85 90 95
Ile Asp Arg Leu Asp Gly Ala His Ala Pro Glu Leu Thr Lys Lys Val
100 105 110
Gln Arg His Ala Ser Ser Gly Ser Phe Leu Pro Ser Ala Asn Glu His
115 120 125

Leu Lys Glu Asp Leu Ser Leu Arg Leu Lys Lys Leu Thr His Ala Ala
130 135 140

Pro Cys Met Leu Phe Met Lys Gly Thr Pro Gln Glu Pro Arg Cys Gly
145 150 155 160

Phe Ser Lys Gln Met Val Glu Ile Leu His Lys His Asn Ile Gln Phe
165 170 175

Ser Ser Phe Asp Ile Phe Ser Asp Glu Glu Val Arg Gln Gly Leu Lys
180 185 190

Thr Tyr Ser Asn Trp Pro Thr Tyr Pro Gln Leu Tyr Val Ser Gly Glu
195 200 205

Leu Ile Gly Gly Leu Asp Ile Ile Lys Glu Leu Glu Ala Ser Glu Glu
210 215 220

Leu Asp Thr Ile Cys Pro Lys Ala Pro Lys Leu Glu Glu Arg Leu Lys
225 230 235 240

Val Leu Thr Asn Lys Ala Ser Val Met Leu Phe Met Lys Gly Asn Lys
245 250 255

Gln Glu Ala Lys Cys Gly Phe Ser Lys Gln Ile Leu Glu Ile Leu Asn
260 265 270

Ser Thr Gly Val Glu Tyr Glu Thr Phe Asp Ile Leu Glu Asp Glu Glu
275 280 285

Val Arg Gln Gly Leu Lys Ala Tyr Ser Asn Trp Pro Thr Tyr Pro Gln
290 295 300

Leu Tyr Val Lys Gly Glu Leu Val Gly Gly Leu Asp Ile Val Lys Glu
305 310 315 320

Leu Lys Glu Asn Gly Glu Leu Leu Pro Ile Leu Arg Gly Glu Asn
325 330 335

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACTTTTTCG ATGCCTACTG GAGACTTTGA TTCGAAGCCC AGTTGGGCCG ACCAGGTGGA 60

GGAGGAGGGG GAGGACGACA AATGTGTAC CAGCGAGCTC CTCAAGGGGA TCCCTCTGGC 120

CACAGGTGAC ACCAGCCCAG AGCCAGAGCT ACTGCCGGGA GCTCCACTGC CGCCTCCCAA 180
GGAGGTCATC AACCGAAACA TAAAGACAGT GACAGAGTAC AAGATAGATG AGGATGGCAA 240
GAAGTTCAAG ATTGTCCGCA CCTTCAGGAT TGAGACCCGG AAGGCTTCAA AGGCTGTCGC 300
AAGGAGGAAG AACTGGAAGA AGTTCGGGAA CTCAGAGTTT GACCCCCCCG GACCCAATGT 360
GGCCACCACC ACTGTCAGTG ACGATGTCTC TATGACGTTT ATCACCAGCA AAGAGGACCT 420
GAACTGCCAG GAGGAGGAGG ACCCTATGAA CAAACTCAAG GGCCAGAAGA TCGTGTCTTG 480
CCGCATCTGC AAGGGCGACC ACTGGACCAC CCGCTGCCCC TACAAGGATA CGCTGGGGCC 540
CATGCAGAAG GAGCTGGCCG AGCAGCTGGG CCTGTCTACT GGCGAGAAGG AGAAGCTGCC 600
GGGAGAGCTA GAGCCGGTGC AGGCCACGCA GAACAAGACA GGAAGTATG TGCCGCCGAG 660
CCTGCGCGAC GGGGCCAGCC GCCGCGGGGA GTCCATGCAG CCCACCCGCA GAGCCGACGA 720
CAACGCCACC ATCCGTGTCA CCAACTTGTC AGAGGACACG CGTGAGACCG ACCTGCAGGA 780
GCTCTTCCGG CCTTTCGGCT CCATCTCCCG CATCTACCTG GCTAAGGACA AGACCACTGG 840
CCAATCCAAG GGCTTCGCCT TCATCAGCTT CCACCGCCGC GAGGATGCTG CGCGTGCCAT 900
TGCCGGGGTG TCCGGCTTTG GCTACGACCA CCTCATCTC AACGTCGAGT GGGCCAAGCC 960
GTCCACCAAC TAAGCCAGCT GCCACCGTGT ACTCGGTCCG GGACCCTTGG CGACAGAAGA 1020
CAGCCTCCGA GAGCGCGGGC TCCAAGGGCA ATAAAGCAGC TCCACTCTCA AAAAAAAAAA 1080
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
AAAAAAAAA AA 1152

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met Pro Thr Gly Asp Phe Asp Ser Lys Pro Ser Trp Ala Asp Gln Val
1 5 10 15

Glu Glu Glu Gly Glu Asp Asp Lys Cys Val Thr Ser Glu Leu Leu Lys
20 25 30

Gly Ile Pro Leu Ala Thr Gly Asp Thr Ser Pro Glu Pro Glu Leu Leu
35 40 45

Pro Gly Ala Pro Leu Pro Pro Pro Lys Glu Val Ile Asn Gly Asn Ile
50 55 60

Lys Thr Val Thr Glu Tyr Lys Ile Asp Glu Asp Gly Lys Lys Phe Lys
65 70 75 80

Ile Val Arg Thr Phe Arg Ile Glu Thr Arg Lys Ala Ser Lys Ala Val
85 90 95

Ala Arg Arg Lys Asn Trp Lys Lys Phe Gly Asn Ser Glu Phe Asp Pro
100 105 110

Pro Gly Pro Asn Val Ala Thr Thr Thr Val Ser Asp Asp Val Ser Met
115 120 125

Thr Phe Ile Thr Ser Lys Glu Asp Leu Asn Cys Gln Glu Glu Glu Asp
130 135 140

Pro Met Asn Lys Leu Lys Gly Gln Lys Ile Val Ser Cys Arg Ile Cys
145 150 155 160

Lys Gly Asp His Trp Thr Thr Arg Cys Pro Tyr Lys Asp Thr Leu Gly
165 170 175

Pro Met Gln Lys Glu Leu Ala Glu Gln Leu Gly Leu Ser Thr Gly Glu
180 185 190

Lys Glu Lys Leu Pro Gly Glu Leu Glu Pro Val Gln Ala Thr Gln Asn
195 200 205

Lys Thr Gly Lys Tyr Val Pro Pro Ser Leu Arg Asp Gly Ala Ser Arg
210 215 220

Arg Gly Glu Ser Met Gln Pro Thr Arg Arg Ala Asp Asp Asn Ala Thr
225 230 235 240

Ile Arg Val Thr Asn Leu Ser Glu Asp Thr Arg Glu Thr Asp Leu Gln
245 250 255

Glu Leu Phe Arg Pro Phe Gly Ser Ile Ser Arg Ile Tyr Leu Ala Lys
260 265 270

Asp Lys Thr Thr Gly Gln Ser Lys Gly Phe Ala Phe Ile Ser Phe His
275 280 285

Arg Arg Glu Asp Ala Ala Arg Ala Ile Ala Gly Val Ser Gly Phe Gly
290 295 300

Tyr Asp His Leu Ile Leu Asn Val Glu Trp Ala Lys Pro Ser Thr Asn
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGAGACCTG GGCTGCTGTG AAAGCCCCTG CACAATCAGC CAGGGAGAAC TGGGCGGGTT	60
TAGTGGCCCC AGGCCCACTC CTCATGCAGC AGTGTGCTGG GGCGACAGCT CGTCTCCCCT	120
CTCTTAAGCA CCCGCTTCCT CACCACCCCC ACTGTTGGGC CTATAGTAGC AGGTTAGTGA	180
GTACCTAGGG CGGCTCAACT CCTCCCACAG CACCAACCCA GCATGGTCCC ACTGAAGTCC	240
TACTACGCCC TCCCCTCCCC AGCCTTTTCC AGAAACCATA CTGGGCTCAG ATCAGAGCTC	300
CGAAGCGGTC AAAGTGAGCT GAGCAGGACA GGCCCAGCCT TTCTCCACTG CCACGTCCCT	360
CATGCACATC ACTCATCTCC TGCTGCAGGC CAAGGCCAAA ATTGGGCTAG TCCTGGCCAG	420
GGAAATCAGA AGCTCTTCTT GGGTGAGATT GAGCCTCCTG TTGCTCCCTG GAGTTCCGGA	480
GGCTGGGCTG CAGCCCCTC AGCTTGCGGG CAAAATACGT GCTCTCCTCT CTCCTTGTC	540
GCTGAGCAAA CCCAGGGAAT AGCCCTCCTC TCCCAGGAA ACTTCTCTGA AATCTTAGAC	600
TTAGCCAGTC TTAGGCCTAC GATGCCACAC AAAGGTTGTT CAGGGAGAAG GGGGTGCAGG	660
AGGCAGAGGG TGCCCCGAG GGAGCTGGTG GCTCCAGCCC CACTAGAGCT CTTAAAGATC	720
ACACAGCAGC TGCTCCTGAC AGGGATGCTC ATGCCAGAA AGCAAGCCCA GGAGAGGAAG	780
GCAGAGTGTG ACAGAGCAGA GCCAGGGCCA GGCGCACCAG GAGAGGCGTT TCTGGGGCTC	840
CAGGGAAGTG CCACGGGAGG CAGAAGTCCA GAACTGCCCC TATAGATGCC CTTCTACATC	900
CTGGAGCCCA AATCAGTCAT GTGGGTGGGA AGTCCCAGG GCAGTGGTCA CATCGTGAGA	960
ATTAGCAGGA AAGGCGGGGC CTTTCTTGTC ATAGCTATTT CTGAGGATGA AATGGGAGAC	1020
ATATGCCAG CACCTGATGT AAGTTTATAT AATGTACCTA CACTAAGAA ATACATGAAC	1080
CGTGCCATGA GGACAGTAAG TGTTCATAAA GCAACATGAA GCAAGAAACA GTGCAGGGTG	1140
CCCAGTGCAC AACTAGAGA GAAATTGTGA ACATTAAGGA CAAGGAGAAT TGGTGTCTTT	1200
CTAAACATA CTTATTTAAA AACACATACC CACTTACTAA TGTGGAATTA CACAGTTTGT	1260
AACAAGAAAA CAGTCTCTCC CATTCTCTAG TACTGYTCCC CTACCCAGCA GTCAMTTCCA	1320
GTTCAATCAG STATTTTAA AATGTGCTTA TATGACTCTT GCTTGATATA TCAATYTTAG	1380

ACATTACCTG TTGACTCCCT GTTGTCTATC ATGAGGCTTT AGCTCTYTTT TGTCAGCAAC 1440
 CCTCCCCCAT CCCTAGTTAT TAGGTTAAAA AATACTCAGA TTACTATTTC TATTACTATG 1500
 TGAAAGTTAA CTGCGGAGCC AAGAGTTGGA CTATAATTAA ATTACCTTCC TTGTAAAAAA 1560
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 1594

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Met Val Pro Leu Lys Ser Tyr Tyr Ala Leu Pro Ser Pro Ala Phe Ser
 1 5 10 15
 Arg Asn His Thr Gly Leu Arg Ser Glu Leu Arg Ser Gly Gln Ser Glu
 20 25 30
 Leu Ser Arg Thr Gly Pro Ala Phe Leu His Cys His Val Pro His Ala
 35 40 45
 His His Ser Ser Pro Ala Ala Gly Gln Gly Gln Asn Trp Ala Ser Pro
 50 55 60
 Gly Gln Gly Asn Gln Lys Leu Phe Leu Gly Glu Ile Glu Pro Pro Val
 65 70 75 80
 Ala Pro Trp Ser Ser Gly Gly Trp Ala Ala Ala His Ser Ala Cys Gly
 85 90 95
 Gln Asn Thr Cys Ser Pro Leu Ser Leu Ser Ala Glu Gln Thr Gln Gly
 100 105 110
 Ile Ala Leu Leu Ser Pro Gly Asn Phe Ser Glu Ile Leu Asp Leu Ala
 115 120 125
 Ser Leu Arg Pro Thr Met Pro His Lys Gly Cys Ser Gly Arg Arg Gly
 130 135 140
 Cys Arg Arg Gln Arg Val Pro Arg Arg Glu Leu Val Ala Pro Ala Pro
 145 150 155 160
 Leu Glu Leu Leu Lys Ile Thr Gln Gln Leu Leu Thr Gly Met Leu
 165 170 175
 Met Pro Arg Lys Gln Ala Gln Glu Arg Lys Ala Glu Cys Asp Arg Ala
 180 185 190

Glu Pro Gly Pro Gly Ala Pro Gly Glu Ala Phe Leu Gly Leu Gln Gly
195 200 205

Ser Ala Thr Gly Gly Arg Ser Pro Glu Leu Pro Ile
210 215 220

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TNAATAAACTG GACGGATGCA CTGATAGG

29

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CNCTGATAACA AAGCATTGCC ACTGGCGC

29

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TNATCCAGAAA ATTACCGCCG TCCGACCG

29

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CNCTTAGAAGC CTTCATTTTG GGAAGTC

29

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CNGAGAAGACT CAACGAGGCA GCCAAGAA

29

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CNTGCTGACTT GGCCAAGAA GCTTGATT

29

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GNGCTGCTTTC CAGACTCCTT CAGTTTCT

29

- (2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ANCCACAGCGT GGTTCCTTGAG GTGTTCCC

29

- (2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonulceotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GNTCTTCTGGC CCTTGAGTTT GTTCATAG

29

- (2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GNTGAGCCGCC CTAGGTACTC ACTAACCT

29

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

AGGCGCCCTC CCTTCCTGAG GAGCTGTTGG CCTGGGTGGG CAGGAACTGC AGTATGGCCA	60
TGGGCTGAGC AGGCTGAGCA CCTCAGCCTT TAGGGCTTAT GGCCAGGGGA CACTGTATGA	120
CTCTCCTCTC CTGCAGGTGT CTATCCACCT GGGGTATGGC ATCTACCGAC CTGTCTCCCT	180
GGGGTCACAT GCTTTGTTTC CATTCTTGTC CTGGCTGGAC CAGCCACTGT GGGACCAACA	240
CCCCTCCCAC ACTCCCCAG ACTGCTCGTC TATCACCAGG ATCGCTTTGT ACTTTGTGCA	300
AAAGGTCTG GCTGTCCCTT GCTGTTTTCA TCTCTGCCAA GCCTATTGTG CCTCTGGCTG	360
CTGTATGTGT GCGCGTGCAC GTGTGTGTGT TTCATCTGTT CATTCACTGC ACAAGATATT	420
TATTGAGTGC CCACTACGTG CCAGGCACTG TTGCTGAGTT CCTGTGGGTG TGTCTCTCGA	480
TGCCACTCCT GCTTCTCTGG GGGCCTCTTT CTGTGCTTCT CTTTGTCCCC AAATTGCTAC	540
CTCTTTGTCA GTCTGGGTGT CTCAGGTTCT GTGTGTCCTT GTGTGCATTT CTGTCTCTCT	600
CTGTCCCTCGT CTCTCTGCAA GGCCCTCTAT TTCTCTCTTT CTTGGTGTCT GTCCTTTGCC	660
CCCTGTGCCC TCTGGATTCT CTGGGTCTAT GTAGGCCCTT GGTCTGCCCT GGGCTCATCA	720
GCCTTCCTGA CCTCCTCCTG CCCTCCCCTT CACTCCCCTC CTGGCTCTGC CAGTCGGTTC	780
CCACGGAGCC ATTTTCTAGCT CTGATCAGCA TGGGAATGTG CCTCGGCCTC CAAGGGGCTT	840
TGTCCTGGTG CCCCCGCCCC TGGTCCCAAC CTGATCCCAC GAGGGAGTTG GGACAGGAGG	900
ATTGATGGTG CTCCCCTTCC TGCCAGCGTC AGAGGCCCTG GAGAGGGGCT GTCCATGGCA	960
GCTGGTCTTT ATTCTCCTT CATGAGCACA GGGTCGGGGG GTCCCCATTC TTGGAAGAGG	1020
TTGAGAAGAC TCCTGGGCTT CAGCCTCTCC CACCCAGCCC TGCCCCTCAC CTGCCTGCCC	1080
TCCCCTCCCC CACTCTATAC TAGGGACTGG ATCTCAGCCT CTGATCAGTT TCACAAAGTT	1140
TGTTCCCTAA GGAAATCAAA TCCCATTGTC ACCTAACTCT GAAGATCTAA ATAGCCCTTG	1200
GATCAGTACG GGAACCCCAA ATCCACAGG GCCAGATGTG GAGTCTGTGT CTGCCCCCGT	1260

CTTCTCTCCA TCCTCAAAGC CCCCACTTCT CTCCAGGCTG TTTCTTTTTT TATGACTGTA 1320
AACATAGATA GTGCTTTATT TTGTTAATAA TAAGATAATG ATGAGTAACT TAACCAGCAC 1380
ATTTCTCCTG TTTACACTCG GGGGATTTTT TTGTTTTCTG ATGACATAAT AAAGACAGAT 1440
CATTTCAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1480

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met	Ala	Arg	Gly	His	Cys	Met	Thr	Leu	Leu	Ser	Cys	Arg	Cys	Leu	Ser	1	5	10	15
Thr	Trp	Gly	Met	Ala	Ser	Thr	Asp	Leu	Ser	Pro	Trp	Gly	His	Met	Leu	20	25	30	
Cys	Phe	His	Ser	Cys	Pro	Gly	Trp	Thr	Ser	His	Cys	Gly	Thr	Asn	Thr	35	40	45	
Pro	Pro	Thr	Leu	Pro	Gln	Thr	Ala	Arg	Leu	Ser	Pro	Gly	Ser	Leu	Cys	50	55	60	
Thr	Leu	Cys	Lys	Arg	Val	Trp	Leu	Ser	Leu	Ala	Val	Phe	Ile	Ser	Ala	65	70	75	80
Lys	Pro	Ile	Val	Pro	Leu	Ala	Ala	Val	Cys	Val	Arg	Val	His	Val	Cys	85	90	95	
Val	Phe	His	Leu	Phe	Ile	His	Cys	Thr	Arg	Tyr	Leu	Leu	Ser	Ala	His	100	105	110	
Tyr	Val	Pro	Gly	Thr	Val	Ala	Glu	Phe	Leu	Trp	Val	Cys	Leu	Ser	Met	115	120	125	
Pro	Leu	Leu	Leu	Leu	Trp	Gly	Pro	Leu	Ser	Val	Leu	Leu	Phe	Val	Pro	130	135	140	
Lys	Leu	Leu	Pro	Leu	Cys	Gln	Ser	Gly	Cys	Leu	Arg	Phe	Cys	Val	Ser	145	150	155	160
Leu	Cys	Ala	Phe	Leu	Ser	Leu	Ser	Val	Leu	Val	Ser	Leu	Gln	Gly	Pro	165	170	175	
Leu	Phe	Leu	Ser	Phe	Leu	Val	Ser	Val	Leu	Cys	Pro	Leu	Cys	Pro	Leu				

180	185	190
Asp Ser Leu Gly Leu Cys Arg Pro Leu Val Cys Pro Gly Leu Ile Ser		
195	200	205
Leu Pro Asp Leu Leu Leu Pro Ser Pro Ser Leu Pro Pro Trp Leu Cys		
210	215	220
Gln Ser Val Pro Thr Glu Pro Phe Leu Ala Leu Ile Ser Met Gly Met		
225	230	235
Cys Leu Gly Leu Gln Gly Ala Leu Ser Trp Cys Pro Arg Pro Trp Ser		
245	250	255
Gln Pro Asp Pro Thr Arg Glu Leu Gly Gln Glu Asp		
260	265	

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CCCCGCGGCT CCTGGAACCC CGGTTTCGCGG CGATGCCAGC CACCCCAGCG AAGCCGCCGC	60
AGTTCAGTGC TTGGATAATT TGAAAGTACA ATAGTTGGTT TCCCTGTCCA CCCGCCCCAC	120
TTCGCTTGCC ATCACAGCAC GCCTATCGGA TGTGAGAGGA GAAGTCCCGC TGCTCGGGCA	180
CTGTCTATAT ACGCCTAACA CCTACATATA TTTTAAAAAC ATTAAATATA ATTAACAATC	240
AAAAGAAAGA GGAGAAAGGA AGGGAAGCAT TACTGGGTTA CTATGCACTT GCGACTGATT	300
TCTTGGCTTT TTATCATTTT GAACTTTATG GAATACATCG GCAGCCAAAA CGCCTCCCGG	360
GGAAGGCGCC AGCGAAGAAT GCATCCTAAC GTTAGTCAAG GCTGCCAAGG AGGCTGTGCA	420
ACATGCTCAG ATTACAATGG ATGTTTGTCA TGTAAGCCCA GACTATTTTT TGCTCTGGAA	480
AGAATTGGCA TGAAGCAGAT TGGAGTATGT CTCTCTTCAT GTCCAAGTGG ATATTATGGA	540
ACTCGATATC CAGATATAAA TAAGTGTAACA AAATGCAAAAG CTGACTGTGA TACCTGTTTC	600
AACAAAAATT TCTGCACAAA ATGTAAAAGT GGATTTTACT TACACCTTGG AAAGTGCCTT	660
GACAATTGCC CAGAAGGGTT GGAAGCCAAC AACCATACTA TGGAGTGTGT CAGTATTGTG	720
CACTGTGAGG TCAGTGAATG GAATCCTTGG AGTCCATGCA CGAAGAAGGG AAAAACATGT	780

GGCTTCAAAA GAGGGACTGA AACACGGGTC CGAGAAATAA TACAGCATCC TTCAGCAAAG 840
 GGTAACCTGT GTCCCCAAC AAATGAGACA AGAAAGTGTA CAGTGCAAAG GAAGAAGTGT 900
 CAGAAGGGAG AACGAGGAAA AAAAGGAAGG GAGAGGAAAA GAAAAAACC TAATAAAGGA 960
 GAAAGTAAAG AAGCAATACC TGACAGCAAA AGTCTGGAAT CCAGCAAAGA AATCCCAGAG 1020
 CAACGAGAAA ACAAACAGCA GCAGAAGAAG CGAAAAGTCC AAGATAAACA GAAATCGGGG 1080
 ATTGAAGTCA CCCTAGCTGA AGGCCTCACC AGTGTTCAC AGAGGACACA GCCCACCCT 1140
 TGCAGGAGGA GGTATCTCTG AGTGTGCAGC ACAGAATCGC ATGACCCACC TTAACCTTCC 1200
 TGTGTTCATG GAAGGATGCA CGGCTGCTCT GTCCACTGTG ATTCCTAGCC CTCTCAAGAT 1260
 CACTGCTTTC TGAAGAATTT GCAATGACTC TGGCTTCTGG CTGCTTATCT CTGGACACCC 1320
 GTTCTCCACC AGTTGTACAG TTCATGTAAT CTAATTGGCT TAATTGATTT TCCACTTCTC 1380
 TCTTCCTCTT CTAAGATATA AACATTTTAA ATGATTTAAA AAAAAAAAAA AAAAAA 1436

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met	His	Leu	Arg	Leu	Ile	Ser	Trp	Leu	Phe	Ile	Ile	Leu	Asn	Phe	Met
1				5				10					15		
Glu	Tyr	Ile	Gly	Ser	Gln	Asn	Ala	Ser	Arg	Gly	Arg	Arg	Gln	Arg	Arg
			20					25					30		
Met	His	Pro	Asn	Val	Ser	Gln	Gly	Cys	Gln	Gly	Gly	Cys	Ala	Thr	Cys
			35				40					45			
Ser	Asp	Tyr	Asn	Gly	Cys	Leu	Ser	Cys	Lys	Pro	Arg	Leu	Phe	Phe	Ala
	50					55				60					
Leu	Glu	Arg	Ile	Gly	Met	Lys	Gln	Ile	Gly	Val	Cys	Leu	Ser	Ser	Cys
65					70				75						80
Pro	Ser	Gly	Tyr	Tyr	Gly	Thr	Arg	Tyr	Pro	Asp	Ile	Asn	Lys	Cys	Thr
			85					90					95		
Lys	Cys	Lys	Ala	Asp	Cys	Asp	Thr	Cys	Phe	Asn	Lys	Asn	Phe	Cys	Thr
			100				105						110		
Lys	Cys	Lys	Ser	Gly	Phe	Tyr	Leu	His	Leu	Gly	Lys	Cys	Leu	Asp	Asn

115	120	125
Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser		
130	135	140
Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr		
145	150	155
Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val		
	165	170
Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro		
	180	185
Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys		
	195	200
Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn		
210	215	220
Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser		
225	230	235
Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys		
	245	250
Arg Lys Val Gln Asp Lys Gln Lys Ser Gly Ile Glu Val Thr Leu Ala		
	260	265
Glu Gly Leu Thr Ser Val Ser Gln Arg Thr Gln Pro Thr Pro Cys Arg		
	275	280
Arg Arg Tyr Leu		
290		

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GGTTAAGAGC AGATTAGAAC AGAAATCAGG AGAACTTGGG AAGAAGATCA CTGAGTTAAC	60
ATTGAAAAAT CAGACACTAC AAAAGGAAAT TGAAAAAGTT TATTTGGATA ATAAGCTCCT	120
CAAGGAGCAA GCACATAACT TAACAATTGA AATGAAAAAT CATTATGTTC CTTTAAAGT	180
AAGTGAAGAC ATGAAAAAGT CACATGATGC AATTATTGAT GATCTTAATA GAAAGCTTTT	240

AGATGTAACA	CAAAAATATA	CAGAAAAGAA	GTTGGAAATG	GAGAAATTGC	TACTGGAAAA	300
TGACAGCTTA	AGTAAGGATG	TAAGCCGCCT	AGAAACTGTG	TTTGTACCTC	CTGAGAAACA	360
TGAAAAAGAG	ATAATAGCTC	TGAAATCCAA	TATTGTTGAA	CTTAAGAAAC	AGCTGTCTGA	420
ACTTAAGAAA	AAATGTGGTG	AAGACCAGGA	GAAAAATACAC	GCTCTCACAT	CTGAAAACAC	480
TAACTTGAAG	AAGATGATGA	GTAATCAGTA	TGTGCCAGTT	AAAACCCATG	AAGAGGTTAA	540
AATGACACTG	AATGACACGT	TAGCCAAAAC	TAACAGAGAA	TTATTAGATG	TGAAGAAAAA	600
ATTTGAAGAT	ATAAATCAGG	AATTTGTAAA	AATAAAAGAT	AAGAATGAAA	TATTA AAAAAG	660
AAACCTGGAA	AACACTCAGA	ACCAAATAAA	AGCTGAGTAC	ATCAGCCTGG	CAGAGCACGA	720
GGCAAAGATG	AGCTCGCTAA	GTCAGAGCAT	GAGAAAGGTG	CAGGATAGTA	ATGCTGAAAT	780
CTTGGCCAAC	TACAGAAAAG	GCCAAGAAGA	GATTGTGACA	CTGCATGCCG	AAATTAAAGC	840
CCAGAAGAAG	GAGCTCGACA	CAATACAAGA	ATGCATTAAG	GTAAAATATG	CCCCAATTGT	900
CAGCTTTGAG	GAGTGCGAGA	GAAAATTTAA	AGCAACAGAG	AAAGAACTAA	AAGACCAGTT	960
ATCAGAGCAG	ACACAAAAGT	ATAGTGTCAG	TGAAGAAGAA	GTCAAGAAAA	ACAAGCAAGA	1020
GAATGACAAG	TTAAAGAAGG	AGATTTTTAC	CCTTCAGAAA	GATTTGAGAG	ATAAGACAGT	1080
TCTCATTGAG	AAGTCTCATG	AAATGGAAAAG	AGCATTAAGC	AGAAAAACAG	ACGAGCTAAA	1140
CAAACAGTTA	AAAGACTTGT	CACAGAAATA	CACGGAAGTA	AAGAATGTGA	AAGAGAAGCT	1200
AGTAGAAGAA	AATGCCAAAC	AGACTTCTGA	GATACTTGCA	GTGCAAAATC	TTTTGCAAAA	1260
ACAACATGTT	CCATTGGAAC	AGGTTGAGGC	TCTGAAAAAA	TCTCTTAATG	GCACAATTGA	1320
AAATCTAAAG	GAAGAACTGA	AGAGTATGCA	AAGGTGTTAC	GAGAAAGAGC	AGCAGACAGT	1380
GACCAAACCTG	CATCAATTGT	TGGAGAATCA	AAAGAACTCT	TCTGTACCCC	TGGCAGAGCA	1440
TTTGACAGATT	AAAGAAGCAT	TTGAGAAAGA	AGTTGGAATC	ATAAAAGCCA	GCTTGAGAGA	1500
AAAGGAAGAA	GAAAGCCAAA	ACAAAATGGA	AGAAGTCTCC	AACTTTCAGT	CGGAGGTTCA	1560
GAATACTAAA	CAAGCATTAA	AAAAATTAGA	GACTAGAGAG	GTAGTTGACT	TGTCTAAATA	1620
TAAAGCAACA	AAAAGTGATT	TGGAGACACA	GATTTCTAGC	TTAAATGAAA	AATTGGCCAA	1680
TCTGAATAGA	AAGTATGAGG	AAGTATGTGA	GGAAGTTTTG	CATGCCAAAA	AGAAGGAAAT	1740
ATCTGCAAAA	GATGAGAAGG	AATTACTGCA	TTTCAGCATT	GAGCAAGAAA	TTAAGGATCA	1800
GAAGGAACGA	TGTGATAAGT	CCTTAACAAC	AATCACAGAG	TTACAAAGAA	GAATACAAGA	1860
ATCTGCTAAA	CAAATAGAAG	CAAAAGATAA	TAAGATAACT	GAAGTGCTTA	ATGATGTGGA	1920
AAGATTAAAA	CAGGCACTCA	ATGGCCTTTC	CCAACCTACC	TACACAAGTG	GGAACCCAC	1980

CAAGAGGCAG AGCCAGCTGA TTGACACTCT GCAGCACCAA GTGAAATCTC TGGAGCAACA 2040
GCTGGCCGAT GCTGACAGAC AGCACCAAGA AGTAATTGCA ATTTATCGGA CACACCTTCT 2100
TAGTGCTGCA CAGGGTCACA TGGATGAAGA TGTTTCAGGAG GCTCTGCTCC AGATCATACA 2160
AATGCGGCAG GGGCTTGTGT GCTAGCCGTT AGCACTGACT GCCAGTATCT GTTTTATCTT 2220
GCTGGTGCTG AACATTCTTT GTGCAACTCC ATGGTCTTTC TGGGCCTTAC TGTGCTGGTA 2280
TAATTAAAAT AAAATATATT TTGTTCTAAA AAAAAAAAAA AA 2322

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met	Lys	Asn	His	Tyr	Val	Pro	Leu	Lys	Val	Ser	Glu	Asp	Met	Lys	Lys	1	5	10	15
Ser	His	Asp	Ala	Ile	Ile	Asp	Asp	Leu	Asn	Arg	Lys	Leu	Leu	Asp	Val	20	25	30	
Thr	Gln	Lys	Tyr	Thr	Glu	Lys	Lys	Leu	Glu	Met	Glu	Lys	Leu	Leu	Leu	35	40	45	
Glu	Asn	Asp	Ser	Leu	Ser	Lys	Asp	Val	Ser	Arg	Leu	Glu	Thr	Val	Phe	50	55	60	
Val	Pro	Pro	Glu	Lys	His	Glu	Lys	Glu	Ile	Ile	Ala	Leu	Lys	Ser	Asn	65	70	75	80
Ile	Val	Glu	Leu	Lys	Lys	Gln	Leu	Ser	Glu	Leu	Lys	Lys	Lys	Cys	Gly	85	90	95	
Glu	Asp	Gln	Glu	Lys	Ile	His	Ala	Leu	Thr	Ser	Glu	Asn	Thr	Asn	Leu	100	105	110	
Lys	Lys	Met	Met	Ser	Asn	Gln	Tyr	Val	Pro	Val	Lys	Thr	His	Glu	Glu	115	120	125	
Val	Lys	Met	Thr	Leu	Asn	Asp	Thr	Leu	Ala	Lys	Thr	Asn	Arg	Glu	Leu	130	135	140	
Leu	Asp	Val	Lys	Lys	Lys	Phe	Glu	Asp	Ile	Asn	Gln	Glu	Phe	Val	Lys	145	150	155	160

Ile Lys Asp Lys Asn Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln
165 170 175

Asn Gln Ile Lys Ala Glu Tyr Ile Ser Leu Ala Glu His Glu Ala Lys
180 185 190

Met Ser Ser Leu Ser Gln Ser Met Arg Lys Val Gln Asp Ser Asn Ala
195 200 205

Glu Ile Leu Ala Asn Tyr Arg Lys Gly Gln Glu Glu Ile Val Thr Leu
210 215 220

His Ala Glu Ile Lys Ala Gln Lys Lys Glu Leu Asp Thr Ile Gln Glu
225 230 235 240

Cys Ile Lys Val Lys Tyr Ala Pro Ile Val Ser Phe Glu Glu Cys Glu
245 250 255

Arg Lys Phe Lys Ala Thr Glu Lys Glu Leu Lys Asp Gln Leu Ser Glu
260 265 270

Gln Thr Gln Lys Tyr Ser Val Ser Glu Glu Glu Val Lys Lys Asn Lys
275 280 285

Gln Glu Asn Asp Lys Leu Lys Lys Glu Ile Phe Thr Leu Gln Lys Asp
290 295 300

Leu Arg Asp Lys Thr Val Leu Ile Glu Lys Ser His Glu Met Glu Arg
305 310 315 320

Ala Leu Ser Arg Lys Thr Asp Glu Leu Asn Lys Gln Leu Lys Asp Leu
325 330 335

Ser Gln Lys Tyr Thr Glu Val Lys Asn Val Lys Glu Lys Leu Val Glu
340 345 350

Glu Asn Ala Lys Gln Thr Ser Glu Ile Leu Ala Val Gln Asn Leu Leu
355 360 365

Gln Lys Gln His Val Pro Leu Glu Gln Val Glu Ala Leu Lys Lys Ser
370 375 380

Leu Asn Gly Thr Ile Glu Asn Leu Lys Glu Glu Leu Lys Ser Met Gln
385 390 395 400

Arg Cys Tyr Glu Lys Glu Gln Gln Thr Val Thr Lys Leu His Gln Leu
405 410 415

Leu Glu Asn Gln Lys Asn Ser Ser Val Pro Leu Ala Glu His Leu Gln
420 425 430

Ile Lys Glu Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala Ser Leu
435 440 445

Arg Glu Lys Glu Glu Glu Ser Gln Asn Lys Met Glu Glu Val Ser Lys
450 455 460

Leu Gln Ser Glu Val Gln Asn Thr Lys Gln Ala Leu Lys Lys Leu Glu
465 470 475 480

Thr Arg Glu Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys Ser Asp
485 490 495

Leu Glu Thr Gln Ile Ser Ser Leu Asn Glu Lys Leu Ala Asn Leu Asn
500 505 510

Arg Lys Tyr Glu Glu Val Cys Glu Glu Val Leu His Ala Lys Lys Lys
515 520 525

Glu Ile Ser Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser Ile Glu
530 535 540

Gln Glu Ile Lys Asp Gln Lys Glu Arg Cys Asp Lys Ser Leu Thr Thr
545 550 555 560

Ile Thr Glu Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln Ile Glu
565 570 575

Ala Lys Asp Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu
580 585 590

Lys Gln Ala Leu Asn Gly Leu Ser Gln Leu Thr Tyr Thr Ser Gly Asn
595 600 605

Pro Thr Lys Arg Gln Ser Gln Leu Ile Asp Thr Leu Gln His Gln Val
610 615 620

Lys Ser Leu Glu Gln Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu
625 630 635 640

Val Ile Ala Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln Gly His
645 650 655

Met Asp Glu Asp Val Gln Glu Ala Leu Leu Gln Ile Ile Gln Met Arg
660 665 670

Gln Gly Leu Val Cys
675

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2041 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

TCTCCCCCT CCCCACACA CACTCACAGG CCGGGCATTG ATGGTAATGT ATGCGAGGAA

60

ACAGCAGAGA CTCAGTGATG GCTGTCACGA CCGGAGGGGG GACTCGCAGC CTTACCAGGC 120
ACTTAAGTAT TCATCGAAGA GTCACCCAG TAGCGGTGAT CACAGACATG AAAAGATGCG 180
AGACGCCGGA GATCCTTCAC CACCAAATAA AATGTTGCGG AGATCTGATA GTCCTGAAAA 240
CAAATACAGT GACAGCACAG GTCACAGTAA GGCCAAAAT GTGCATACTC ACAGAGTTAG 300
AGAGAGGGAT GGTGGGACCA GTTACTCTCC ACAAGAAAAT TCACACAACC ACAGTGCTCT 360
TCATAGTTCA AATTCACATT CTTCTAATCC AAGCAATAAC CCAAGCAAAA CTTCAGATGC 420
ACCTTATGAT TCTGCAGATG ACTGGTCTGA GCATATTAGC TCTTCTGGGA AAAAGTACTA 480
CTACAATTGT CGAACAGAAG TTTCAACAATG GGAAAAACCA AAAGAGTGGC TTGAAAGAGA 540
ACAGAGACAA AAAGAAGCAA ACAAGATGGC AGTCAACAGC TTCCCAAAAG ATAGGGATTA 600
CAGAAGAGAG GTGATGCAAG CAACAGCCAC TAGTGGGTTT GCCAGTGGA AATCTACATC 660
AGGAGACAAA CCCGTATCAC ATTCTTGAC AACTCCTTCC ACGTCTTCTG CCTCTGGACT 720
GAACCCACA TCTGCACCTC CAACATCTGC TTCAGCGGTC CCTGTTTCTC CTGTTCCACA 780
GTCGCCAATA CCTCCCTTAC TTCAGGACCC AAATCTTCTT AGACAATTGC TTCCTGCTTT 840
GCAAGCCACG CTGCAGCTTA ATAATTCTAA TGTGGACATA TCTAAAATAA ATGAAGTTCT 900
TACAGCAGCT GTGACACAAG CCTCACTGCA GTCTATAATT CATAAGTTTC TTACTGCTGG 960
ACCATCTGCT TTCAACATAA CGTCTCTGAT TTCTCAAGCT GCTCAGCTCT CTACACAAGC 1020
CCAGCCATCT AATCAGTCTC CGATGTCTTT AACATCTGAT GCGTCATCCC CAAGATCATA 1080
TGTTTCTCCA AGAATAAGCA CACCTCAAAC TAACACAGTC CCTATCAAAC CTTTGATCAG 1140
TACTCCTCCT GTTTCATCAC AGCCAAAGGT TAGTACTCCA GTAGTTAAGC AAGGACCAGT 1200
GTCACAGTCA GCCACACAGC AGCCTGTAAC TGCTGACAAG CAGCAAGGTC ATGAACCTGT 1260
CTCTCCTCGA AGTCTTCAGC GCTCAAGCCA GAGAAGTCCA TCACCTGGTC CCAATCATAC 1320
TTCTAATAGT AGTAATGCAT CAAATGCAAC AGTTGTACCA CAGAATTCTT CTGCCCCGATC 1380
CACGTGTTCA TTAACGCCTG CACTAGCAGC AACTTCAGT GAAAATCTCA TAAAACACGT 1440
TCAAGGATGG CCTGCAGATC ATGCAGAGAA GCAGGCATCA AGATTACGCG AAGAAGCGCA 1500
TAACATGGGA ACTATTCACTA TGTCCGAAAT TTGTACTGAA TTAATAAATT TAAGATCTTT 1560
AGTCCGAGTA TGTGAAATTC AAGCAACTTT GCGAGAGCAA AGGATACTAT TTTTGAGACA 1620
ACAAATTAAG GAACTTGAAA AGCTAAAAAA TCAGAATTCC TTCATGGTGT GAAGATGTGA 1680
ATAATTGCAC ATGGTTTTGA GAACAGGAAC TGTAATCTG TTGCCCAATC TTAACATTTT 1740

TGAGCTGCAT TTAAGTAGAC TTTGGACCGT TAAGCTGGGC AAAGGAAATG ACAAGGGGAC 1800
 GGGGTCTGTG AGAGTCAATT CAGGGGAAAG ATACAAGATT GATTGTGAAA ACCCTTGAAA 1860
 TGTAGATTTC TTGTAGATGT ATCCTTCACG TTGTAAATAT GTTTTGTAGA GTGAAGCCAT 1920
 GGGAAGCCAT GTGTAACAGA GCTTAGACAT CCAAACTAA TCAATGCTGA GGTGGCTAAA 1980
 TACCTAGCCT TTTACATGTA AACCTGTCTG CAAAATTAGC TTTTAAATAA AAAAAAAAAA 2040
 A 2041

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Met Arg Gly Asn Ser Arg Asp Ser Val Met Ala Val Thr Thr Gly Gly
 1 5 10 15
 Gly Thr Arg Ser Leu Thr Arg His Leu Ser Ile His Arg Arg Val Thr
 20 25 30
 Pro Val Ala Val Ile Thr Asp Met Lys Arg Cys Glu Thr Pro Glu Ile
 35 40 45
 Leu His His Gln Ile Lys Cys Cys Gly Asp Leu Ile Val Leu Lys Thr
 50 55 60
 Asn Thr Val Thr Ala Gln Val Thr Val Arg Pro Lys Met Cys Ile Leu
 65 70 75 80
 Thr Glu Leu Glu Arg Gly Met Val Gly Pro Val Thr Leu His Lys Lys
 85 90 95
 Ile His Thr Thr Thr Val Leu Phe Ile Val Gln Ile His Ile Leu Leu
 100 105 110
 Ile Gln Ala Ile Thr Gln Ala Lys Leu Gln Met His Leu Met Ile Leu
 115 120 125
 Gln Met Thr Gly Leu Ser Ile Leu Ala Leu Leu Gly Lys Ser Thr Thr
 130 135 140
 Thr Ile Val Glu Gln Lys Phe His Asn Gly Lys Asn Gln Lys Ser Gly
 145 150 155 160
 Leu Lys Glu Asn Arg Asp Lys Lys Lys Gln Thr Arg Trp Gln Ser Thr

165

170

175

Ala Ser Gln Lys Ile Gly Ile Thr Glu Glu Arg
180 185

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1163 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GCCCTATCCA CTTAATAGAT GCCAATTC AA AGAGGTTAAA TGATTAGACT AAGGCACCTA 60
 ACTTATGTGA GTGTCAGGCT TCAATGCCTG TGTTAGAGCT ACTCCTTCAC ACAAATAGT 120
 TCAGAACATA GAGAAGGACC AAGGTTAATA AATGATTTTC ATCCCAAACA CTAAACATGA 180
 TTGATGGGTA GAGGCTGCCC GAAGTACTGT GTAAAGATGG AATCTGAGAT AGAAGAATGC 240
 TGTGGTCAAT TAGTAATTCT TGCCCATGGA GGGATTAGTG ACACATGCCT TGTATATTTG 300
 TCATCTGTGG CCTAAACTCT GCCCCTGAAG GTTTGTTTTT TAATTCAGAG GTTTAAATTA 360
 ATCTAGCCCA CTTAATAAAA CCAGAGATCC TATGGGAAAT TTAGCCTAAG ACAGTGCTGG 420
 AAATTGCCAT ATGTTGATAC AAAGAAGTGT TTGGCCACAT TACAGGTCTC AGACTCAACT 480
 GCTATGTGTG ACTGCCGCTC TGTGCCTATG TCTTGCTTTT TTGCTGAGTT CCCTATTTCC 540
 ATATCTCCAG GTGAATCCAT GAGAAGCGAG AGGGTGGCTG AGAGGCCTGG GCCTCTGGGA 600
 TTCCACCTTG CTATCTCTGC TCTTCAACCA TTGTTTTAGA CTCTGAACAC CAGATCCTCA 660
 TATCTGAAAG TGATTTGGAG ACCTGGGCAT CAAGTGCTCT TTTAAGAAGG GGCTATCCCA 720
 GAGGACTGTT CAAAAGTCTC ATTCAATAGA GATGTTGGAG TCCCAGAACA AAGTTAGGGA 780
 GCAAACCACT AACCTATGCT GGTSGTAACA GAGGATCCTA CAATTACGTT TGTTTTTAAG 840
 ACAGGATTTT GCTGTGTTGC CCAGACTGGT CTCAAATCC TGGGTTCAAG AGATCCATCC 900
 TCCCACCTCA GTCTCCTGAA AGCTGGGATG ACAGGCACAT GCCACCACAC CTAGCTCCTT 960
 ACAACCATTT ATTTTAACTT ATTTCAATTA TAACTGGTAT CTTTCATTTG TATGTGGCAG 1020
 CTAGAGATTT ATATAGGATG GAAGTAATTT ATTTTAAATT TAAATATTTT ATGTTGAAC 1080
 GTTTCCTTG TATGGAACAT TTTACTTGGC CAATTCAAAT AAAAATAAAG TCAGCTTTGT 1140

TTGTGACAAA AAAAAAAAAA AAA

1163

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Leu	Ile	Gln	Arg	Ser	Val	Trp	Pro	His	Tyr	Arg	Ser	Gln	Thr	Gln
1				5				10					15		
Leu	Leu	Cys	Val	Thr	Ala	Ala	Leu	Cys	Leu	Cys	Leu	Ala	Phe	Leu	Leu
			20				25						30		
Ser	Ser	Leu	Phe	Pro	Tyr	Leu	Gln	Val	Asn	Pro					
			35				40								

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3067 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GCGGTGGCTG	AGGCGGCTGG	GCCTAGGGTG	CAGCGGGCGC	GTCTGCGGCT	GGTGTGGCG	60
CATCTCTAGA	TCCTTTCCCG	GAGTTCAGTT	ATGGGTGTGA	GAGGTTTGCA	AGGATTTGTG	120
GGAAGTACCT	GCCCACATAT	ATGTACAGTA	GTAAATTTCA	AAGAACTGGC	AGAGCACCAC	180
CGAAGCAAGT	ATCCTGGATG	TACCCCTACC	ATTGTGGTTG	ATGCCATGTG	TTGTCTCAGA	240
TATTGGTATA	CTCCAGAATC	TTGGATCTGC	GGTGGCCAGT	GGCGAGAATA	CTTTTCTGCT	300
TTGCGAGATT	TTGTAAAC	TTTTACGGCA	GCTGGGATCA	AGTTGATATT	CTTCTTTGAT	360
GGCATGGTGG	AGCAGGATAA	GAGAGATGAA	TGGGTGAAAC	GAAGGCTCAA	GAACAACAGG	420
GAGATATCCA	GGATTTTCA	TTACATCAAG	TCACACAAGG	AGCAGCCAGG	CAGAAATATG	480
TTCTTCATCC	CCTCAGGGCT	AGCTGTGTTT	ACACGATTTG	CTCTAAAGAC	ACTGGGCCAG	540
GAAACTTTGT	GTTCTTTGCA	GGAAGCAGAT	TATGAGGTAG	CTTCCTATGG	CCTCCAGCAT	600

AACTGTCTTG GGATTCTGGG GGAAGACACT GATTACCTAA TCTATGACAC TTGTCCCTAC 660

TTTTCAATTA GCGAGCTCTG CCTAGAGAGC CTGGACACCG TCATGCTCTG CAGAGAGAAG 720

CTCTGTGAGA GTCTGGGCCT CTGTGTGGCC GACCTTCCTC TTCTGGCCTG CCTCCTTGGC 780

GACGACATAA TCCCAGAGGG CATGTTTGAA AGCTTTAGGT ACAAATGCTT ATCGTCCTAC 840

ACCTCTGTAA AAGAGAACTT TGACAAAAAA GGTAACATCA TATTAGCTGT GTCAGACCAT 900

ATATCGAAAG TTCTTTACTT GTATCAAGGT GAGAAAAAAT TAGAAGAGAT ATTACCTCTG 960

GGACCAAACA AAGCTCTTTT TTATAAAGGA ATGGCATCAT ATCTTTTACC AGGACAAAAA 1020

TCTCCATGGT TTTTCCAAA ACCCAAAGGT GTAATAACTT TGGACAAACA AGTAATATCC 1080

ACGAGTTCAG ACGCCGAATC CAGGGAAGAA GTTCCCATGT GTTCAGATGC TGAATCCAGG 1140

CAAGAAGTTC CCATGTGTAC AGGCCCTGAA TCCAGGCGAG AAGTTCCCGT GTATACAGAT 1200

TCTGAACCCA GGCAAGAAGT TCCCATGTGT TCAGACCCTG AACCAGGCA AGAAGTTCCC 1260

ACATGTACAG GCCCTGAATC CAGGCGAGAA GTTCCCATGT GTTCAGACCC TGAACCCAGG 1320

CAAGAAGTTC CCATGTGTAC AGGCCCTGAA GCCAGGCAAG AAGTTCCCAT GTATACAGAC 1380

TCTGAACCCA GGCAAGAAGT TCCCATGTAT ACAGACTCTG AACCAGGCA AGAAGTTCCC 1440

ATGTATACAG GCTCTGAACC CAGGCAAGAA GTTCCCATGT ATACAGGCC TGAATCCAGG 1500

CAAGAAGTTC CCATGTATAC AGGCCCTGAA TCCAGGCAAG AAGTTTTAAT ACGGACAGAC 1560

CCTGAATCTA GGCAAGAAAT TATGTGTACA GGCCATGAAT CCAAACAGGA AGTTCCCAT 1620

TGTACAGATC CTATATCCAA GCAAGAAGAC TCCATGTGTA CACACGCTGA AATCAATCAA 1680

AAATTACCTG TAGCAACAGA TTTTGAATTT AAGCTAGAAG CTCTCATGTG TACAAACCTT 1740

GAAATTAAAC AAGAAGACCC CACAAATGTG GGCCTGAAG TAAAGCAACA AGTAACCATG 1800

GTTTCAGACA CTGAAATCTT AAAGGTTGCT AGAACACATC ACGTCCAAGC AGAAAGCTAC 1860

CTGGTGTACA ACATCATGAG CAGTGGAGAG ATTGAATGCA GCAACACCCT AGAAGATGAG 1920

CTTGACCAGG CCTTACCCAG CCAGGCCTTC ATTTACCGTC CCATTCGACA GCGGGTCTAC 1980

TCACTCTTAC TGGAGGACTG TCAAGATGTC ACCAGCACCT GCCTAGCTGT CAAGGAGTGG 2040

TTTGTGTATC CTGGGAACCC ACTGAGGCAC CCGGACCTCG TCAGGCCGCT GCAGATGACC 2100

ATTCCAGGGG GAACGCCTAG TTTGAAAATA TTATGGCTGA ACCAAGAGCC AGAAATACAG 2160

GTTCGGCGCT TGGACACACT CCTAGCCTGT TTCAATCTTT CCTCCTCAAG AGAAGAGCTG 2220

CAGGCTGTCTG AAAGCCCATT TCAAGCTTTG TGCTGCCTCT TGATCTACCT CTTTGTCCAG 2280

GTGGACACGC TTTGCCTGGA GGATTTGCAT GCGTTTATTG CGCAGGCCTT GTGCCTCCAA 2340
 GGAAAATCCA CCTCGCAGCT TGTAATCTA CAGCCTGATT ACATCAACCC CAGAGCCGTG 2400
 CAGCTGGGCT CCCTTCTCGT CCGCGGCCTC ACCACTCTGG TTTTAGTCAA CAGCGCATGT 2460
 GGCTTCCCCT GGAAGACGAG TGATTTTCATG CCCTGGAATG TATTTGACGG GAAGCTTTTT 2520
 CATCAGAAGT ACTTGCAATC TGAAAAGGGT TATGCTGTGG AGGTTCTTTT AGAACAAAAT 2580
 GGAGGTGGGG AAGACAGGGC TCCAGCTACC ACAGGACGGG CTCTGGGTAT AGCCGTTCCA 2640
 GTCAGGGACA GCCGTGGAGA GACCAGGGAC CAGGAAGCAG ACAGTATGAG CATGACCAGT 2700
 GGAGAAGGTA CTAGTCAACC TCCAGAAAAGA GTATGGAGAG AAAAAGAGGC ACACCTGGAC 2760
 GCAGAGCCCT GCCAGCGCCC TCCTCTGCTG TTGCAGCTGC AAGGAGACCA TGCCTGTGGG 2820
 AGCCAGGCCT CGCTTGCATG AAGAAGGAAC GATGCCTTTT TCAATGGTGT CTCCCTCCCA 2880
 TTGTGCAGAA GAGCTTTTGT TGGCTTCTCT CCCGAGCTTG TGCCTGATTC TGTGGCCCAA 2940
 AACAATCATT GTTAACATCT TCATGTGTTT CATTCTGATC TTTCATTCAT ATATATGATG 3000
 CCTAGCTAAT TTCATTTTAA AATAAATGGG AATCTGTTGT AAAAAAAAAA AAAAAAAAAA 3060
 AAAAAAA 3067

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Met	Gly	Val	Arg	Gly	Leu	Gln	Gly	Phe	Val	Gly	Ser	Thr	Cys	Pro	His
1				5				10						15	
Ile	Cys	Thr	Val	Val	Asn	Phe	Lys	Glu	Leu	Ala	Glu	His	His	Arg	Ser
			20					25						30	
Lys	Tyr	Pro	Gly	Cys	Thr	Pro	Thr	Ile	Val	Val	Asp	Ala	Met	Cys	Cys
		35					40					45			
Leu	Arg	Tyr	Trp	Tyr	Thr	Pro	Glu	Ser	Trp	Ile	Cys	Gly	Gly	Gln	Trp
	50					55					60				
Arg	Glu	Tyr	Phe	Ser	Ala	Leu	Arg	Asp	Phe	Val	Lys	Thr	Phe	Thr	Ala
65					70					75					80

Ala Gly Ile Lys Leu Ile Phe Phe Phe Asp Gly Met Val Glu Gln Asp
85 90 95

Lys Arg Asp Glu Trp Val Lys Arg Arg Leu Lys Asn Asn Arg Glu Ile
100 105 110

Ser Arg Ile Phe His Tyr Ile Lys Ser His Lys Glu Gln Pro Gly Arg
115 120 125

Asn Met Phe Phe Ile Pro Ser Gly Leu Ala Val Phe Thr Arg Phe Ala
130 135 140

Leu Lys Thr Leu Gly Gln Glu Thr Leu Cys Ser Leu Gln Glu Ala Asp
145 150 155 160

Tyr Glu Val Ala Ser Tyr Gly Leu Gln His Asn Cys Leu Gly Ile Leu
165 170 175

Gly Glu Asp Thr Asp Tyr Leu Ile Tyr Asp Thr Cys Pro Tyr Phe Ser
180 185 190

Ile Ser Glu Leu Cys Leu Glu Ser Leu Asp Thr Val Met Leu Cys Arg
195 200 205

Glu Lys Leu Cys Glu Ser Leu Gly Leu Cys Val Ala Asp Leu Pro Leu
210 215 220

Leu Ala Cys Leu Leu Gly Asp Asp Ile Ile Pro Glu Gly Met Phe Glu
225 230 235 240

Ser Phe Arg Tyr Lys Cys Leu Ser Ser Tyr Thr Ser Val Lys Glu Asn
245 250 255

Phe Asp Lys Lys Gly Asn Ile Ile Leu Ala Val Ser Asp His Ile Ser
260 265 270

Lys Val Leu Tyr Leu Tyr Gln Gly Glu Lys Lys Leu Glu Glu Ile Leu
275 280 285

Pro Leu Gly Pro Asn Lys Ala Leu Phe Tyr Lys Gly Met Ala Ser Tyr
290 295 300

Leu Leu Pro Gly Gln Lys Ser Pro Trp Phe Phe Gln Lys Pro Lys Gly
305 310 315 320

Val Ile Thr Leu Asp Lys Gln Val Ile Ser Thr Ser Ser Asp Ala Glu
325 330 335

Ser Arg Glu Glu Val Pro Met Cys Ser Asp Ala Glu Ser Arg Gln Glu
340 345 350

Val Pro Met Cys Thr Gly Pro Glu Ser Arg Arg Glu Val Pro Val Tyr
355 360 365

Thr Asp Ser Glu Pro Arg Gln Glu Val Pro Met Cys Ser Asp Pro Glu
370 375 380

Pro Arg Gln Glu Val Pro Thr Cys Thr Gly Pro Glu Ser Arg Arg Glu
385 390 395 400

Val Pro Met Cys Ser Asp Pro Glu Pro Arg Gln Glu Val Pro Met Cys
405 410 415

Thr Gly Pro Glu Ala Arg Gln Glu Val Pro Met Tyr Thr Asp Ser Glu
420 425 430

Pro Arg Gln Glu Val Pro Met Tyr Thr Asp Ser Glu Pro Arg Gln Glu
435 440 445

Val Pro Met Tyr Thr Gly Ser Glu Pro Arg Gln Glu Val Pro Met Tyr
450 455 460

Thr Gly Pro Glu Ser Arg Gln Glu Val Pro Met Tyr Thr Gly Pro Glu
465 470 475 480

Ser Arg Gln Glu Val Leu Ile Arg Thr Asp Pro Glu Ser Arg Gln Glu
485 490 495

Ile Met Cys Thr Gly His Glu Ser Lys Gln Glu Val Pro Ile Cys Thr
500 505 510

Asp Pro Ile Ser Lys Gln Glu Asp Ser Met Cys Thr His Ala Glu Ile
515 520 525

Asn Gln Lys Leu Pro Val Ala Thr Asp Phe Glu Phe Lys Leu Glu Ala
530 535 540

Leu Met Cys Thr Asn Pro Glu Ile Lys Gln Glu Asp Pro Thr Asn Val
545 550 555 560

Gly Pro Glu Val Lys Gln Gln Val Thr Met Val Ser Asp Thr Glu Ile
565 570 575

Leu Lys Val Ala Arg Thr His His Val Gln Ala Glu Ser Tyr Leu Val
580 585 590

Tyr Asn Ile Met Ser Ser Gly Glu Ile Glu Cys Ser Asn Thr Leu Glu
595 600 605

Asp Glu Leu Asp Gln Ala Leu Pro Ser Gln Ala Phe Ile Tyr Arg Pro
610 615 620

Ile Arg Gln Arg Val Tyr Ser Leu Leu Leu Glu Asp Cys Gln Asp Val
625 630 635 640

Thr Ser Thr Cys Leu Ala Val Lys Glu Trp Phe Val Tyr Pro Gly Asn
645 650 655

Pro Leu Arg His Pro Asp Leu Val Arg Pro Leu Gln Met Thr Ile Pro
660 665 670

Gly Gly Thr Pro Ser Leu Lys Ile Leu Trp Leu Asn Gln Glu Pro Glu
675 680 685

Ile Gln Val Arg Arg Leu Asp Thr Leu Leu Ala Cys Phe Asn Leu Ser
690 695 700

Ser Ser Arg Glu Glu Leu Gln Ala Val Glu Ser Pro Phe Gln Ala Leu
705 710 715 720

Cys Cys Leu Leu Ile Tyr Leu Phe Val Gln Val Asp Thr Leu Cys Leu
725 730 735

Glu Asp Leu His Ala Phe Ile Ala Gln Ala Leu Cys Leu Gln Gly Lys
740 745 750

Ser Thr Ser Gln Leu Val Asn Leu Gln Pro Asp Tyr Ile Asn Pro Arg
755 760 765

Ala Val Gln Leu Gly Ser Leu Leu Val Arg Gly Leu Thr Thr Leu Val
770 775 780

Leu Val Asn Ser Ala Cys Gly Phe Pro Trp Lys Thr Ser Asp Phe Met
785 790 795 800

Pro Trp Asn Val Phe Asp Gly Lys Leu Phe His Gln Lys Tyr Leu Gln
805 810 815

Ser Glu Lys Gly Tyr Ala Val Glu Val Leu Leu Glu Gln Asn Gly Gly
820 825 830

Gly Glu Asp Arg Ala Pro Ala Thr Thr Gly Arg Ala Leu Gly Ile Ala
835 840 845

Val Pro Val Arg Asp Ser Arg Gly Glu Thr Arg Asp Gln Glu Ala Asp
850 855 860

Ser Met Ser Met Thr Ser Gly Glu Gly Thr Ser Gln Pro Pro Glu Arg
865 870 875 880

Val Trp Arg Glu Lys Glu Ala His Leu Asp Ala Glu Pro Cys Gln Arg
885 890 895

Pro Pro Leu Leu Leu Gln Leu Gln Gly Asp His Ala Cys Gly Ser Gln
900 905 910

Ala Ser Leu Ala
915

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AGCTGTCTGC TCTCCTGGCA GGAATCGCTG AGGGAGGGAA ACGCGGCTCT GAATCAGCCC	60
AGAACGAGCC TTCGGGAAGC TCACCCTCCG ATCTCGGTGT GATTGTTGTG ATTGTTGTGA	120
TTTCCTGTCT CGTTTGCCTT GACCGCCATG TGAAAGAATC TGTTCCCCAG CTAGGTGGGG	180
AAAATTACACA GGTGGGCTGT CTGTAGAGAG AACTGGCTGA TTAAAGGCTT CTCGTCCCGA	240
TTTTGTGATA GCCAAGTGCT TGGCCTGGTC GACGGTCTTT GCTCCTTTAC AAATAAAGTG	300
TTCTGTTTCA GTTCGTCCCA AGTTTTCAT GAAGGGCAGT GGTTCCTGA CCTCCCAGGT	360
GCCTGGGCTT CCCCAGGTTT CTGATCTGGG GCTTGGGGCC CTGTGTTTGG GGATCGTGGC	420
ACTGTGTGCA CCAGCCTGGA AGCACTGGGC CAGTCTTGGC CAAGCTTTCC ATCAGGGATG	480
ATTTGATCTT GGTGCTACAG GTCTGTGGTA CGACCATTGT TCCACACCAC ATGTCATTAA	540
TAATGCTTCC CATGCTTCTG CTTGCAAATG ACCAGCCTTC CAAACAGCCA GAGCTGTTTC	600
GAGGTGTTTC TGCAGGCAGG TGCAGGCGTG CCCTCAAATA AGCTTTGCCA ATGGAGTCTC	660
AGCAAGAGCA AAACCTGGTC AGGAAAGACA AAGCCTGGGA ATCCACCCCC ATGCCCTGCA	720
GGTTGGCTGG CCCTGGAGCC ATTTATTATA GTGCTAATCA TGTTTCTAGG CAGGTGCAGA	780
TGGCAAGGGC AGTGTCTTGG TGAGCTTTTT AGCACGAAGA GCCAGGTCTG TCGAAGCCTT	840
TGTGAGAGCT GGAAACGCAG GTGTGCTGGG CATGCGCAGT ATGGGGTTTC GGGCTCAGGG	900
CTTGCCCTTT GGCATCAGAC AGACCTGGCT TCGCATCCTG GATTGCTTC TGACGTGCAC	960
CCTTCCCTTT GGGTCTCGTG ATGTGAAATG GAGATGTTGT CATTTGTGAG GGCTCCATGA	1020
AGTTTCGTTG AAATGACAAA TACTAATTTT TTCATCTGTG AAATGGAGAT AATAGTGCTG	1080
ACCTCAGAAC AGCTGAGAGG ACTAAATGAA ATGATGTTGG ATGTAGCCAT AAAGAACGAA	1140
GTCAGGCACT GGTGCACGCC TGGAATCCCA GCTCTTGGGA GACCGAGACA GGTGGATTGC	1200
TTGAGCTCAG GAGTTTGAGA CCAGCCTGAG CAACATAGGG AGGTCCAGTC TCTACAAAAA	1260
ATATGAAAAG TAGCTGGGCG TGGTGGCGCA TGCCTGTAGT CCCACTACTT GGAAGGCTTC	1320
GTTGGGAGGA TCACTTGAGC CCAGAAGATT GAGGCTGCAG TAAGCCGTGA TCGTGCCACT	1380
GCATTCCAGC CTGGGCAACA GAGCGAGACA CTGTCTCAAA TAAAAAAGAT GGGGAATAGTA	1440
GACACTGGGG GCTCCAGAAG GAGGGAGGGA GGGAGGAAGG GGAGGAAGGG CTGAAATGCT	1500
TTCTATTGGA TACTATCTGG GCATATTACT TCCTGTGGTT CACTGTCTGG GTGACAGGAT	1560
TCATAGAAGC CCAAACCTTTA GCACCACGCA GCATACCCTT GTAACAAAGC CGCACACGTA	1620
CGCCCTCAAG CTAAAACAAA AGTGGACCGG GAGGCCGAGG TCGGGGGATC ATGAGGTCAG	1680

GAGTTTGAGA CCAGCCTGGC AGATAACGGT GAAACCCCGT CTCTACTAAA AATACCAAAA 1740
 AAAGTTAGCC GGACATGGTG GCAGGTGCCT GTAGTCCCAG CTACTTGGGA GGCTGGGGCA 1800
 GAAGAATCGC TTGAACCCAG GAGGCGGAGG TTGCAGTGAG CCGAGATTGC GCCACTGCAC 1860
 TCCAGCCTGT GCGACAGAGT GAGACTCCGT CTCAAAAAAA AAAAAAAAAA AAAA 1914

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Thr	Ser	Leu	Pro	Asn	Ser	Gln	Ser	Cys	Phe	Glu	Val	Phe	Leu	Gln	1	5	10	15
Ala	Gly	Ala	Gly	Val	Pro	Ser	Asn	Lys	Leu	Cys	Gln	Trp	Ser	Leu	Ser	20	25	30	
Lys	Ser	Lys	Thr	Trp	Ser	Gly	Lys	Thr	Lys	Pro	Gly	Asn	Pro	Pro	Pro	35	40	45	
Cys	Pro	Ala	Gly	Trp	Leu	Ala	Leu	Glu	Pro	Phe	Ile	Ile	Val	Leu	Ile	50	55	60	
Met	Phe	Leu	Gly	Arg	Cys	Arg	Trp	Gln	Gly	Gln	Cys	Leu	Gly	Glu	Leu	65	70	75	80
Phe	Ser	Thr	Lys	Ser	Gln	Val	Cys	Arg	Ser	Leu	Cys	Glu	Ser	Trp	Lys	85	90	95	
Arg	Arg	Cys	Ala	Gly	His	Ala	Gln	Tyr	Gly	Val	Ser	Gly	Ser	Gly	Leu	100	105	110	
Ala	Leu	Trp	His	Gln	Thr	Asp	Leu	Ala	Ser	His	Pro	Gly	Phe	Ala	Ser	115	120	125	
Asp	Val	His	Pro	Ser	Leu	Trp	Val	Ser	130	135									

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 575 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```

CCGACTCCCT TCTTTATGGC GTCGCTCCTG TGCTGTGGGC CGAAGCTGGC CGCCTGCGGC      60
ATCGTCCTCA GCGCCTGGGG AGTGATCATG TTGATAATGC TCGGAATATT TTTCAATGTC      120
CATTCCGCTG TGTTGATTGA GGACGTTCCC TTCACGGAGA AAGATTTTGA GAATGGCCCC      180
CAGAACATAT ACAACCTTTA CGAGCAAGTC AGCTACAAC TTTTCATCGC TGCAGGCCTT      240
TACCTCCTCC TCGGAGGCTT CTCTTTCTGC CAAGTTCGGC TCAATAAGCG CAAGGAATAC      300
ATGGTGCGCT AGGGCCCCGG CGCGTTTCCC CGCTCCAGCC CCTCCTCTAT TTAAAGACTC      360
CCTGCACCGT GTCACCCAGG TCGCGTCCCA CCCTTGCCGG CGCCCTCTGT GGGACTGGGT      420
TTCCCGGGCG AGAGACTGAA TCCCTTCTCC CATCTCTGGC ATCCGGCCCC CGTGGAGAGG      480
GCTGAGGCTG GGGGGCTGTT CCGTCTCTCC ACCCTTCGCT GTGTCCCGTA TCTCAATAAA      540
GAGAATCTGC TCTCTTCAAA AAAAAAAAAA AAAAAA      575

```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
1           5           10          15
Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
20          25          30
Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
35          40          45
Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln
50          55          60
Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
65          70          75          80
Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met

```

85

90

95

Val Arg

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GNAGCCCAGGA GTCTTCTCAA CCTCTTCC

29

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ANCAGTCGCAA GTGCATAGTA ACCCAGTA

29

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TNCTCAGCTTT TATTTGGTTC TGAGTGTT

29

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TNTGCTCAGAC CAGTCATCTG CAGAATCA

29

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

TNCAGCACTGT CTTAGGCTAA ATTTCCCA

29

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GNATTCGGCGT CTGAACTCGT GGATATTA

29

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

ANATGCCCAGA TAGTATCCAA TAGAAAGC

29

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CNACAGCACAG GAGCGACGCC ATAAAGAA

29

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Val Met Tyr Ala Arg Lys Gln Gln Arg Leu Ser Asp Gly Cys His
1 5 10 15

Asp Arg Arg Gly Asp Ser Gln Pro Tyr Gln Ala Leu Lys Tyr Ser Ser
20 25 30

Lys Ser His Pro Ser Ser Gly Asp His Arg His Glu Lys Met Arg Asp
35 40 45

Ala Gly Asp Pro Ser Pro Pro Asn Lys Met Leu Arg Arg Ser Asp Ser
50 55 60

Pro Glu Asn Lys Tyr Ser Asp Ser Thr Gly His Ser Lys Ala Lys Asn
65 70 75 80

Val His Thr His Arg Val Arg Glu Arg Asp Gly Gly Thr Ser Tyr Ser
85 90 95

Pro Gln Glu Asn Ser His Asn His Ser Ala Leu His Ser Ser Asn Ser
100 105 110

His Ser Ser Asn Pro Ser Asn Asn Pro Ser Lys Thr Ser Asp Ala Pro
115 120 125

Tyr Asp Ser Ala Asp Asp Trp Ser Glu His Ile Ser Ser Ser Gly Lys
130 135 140

Lys Tyr Tyr Tyr Asn Cys Arg Thr Glu Val Ser Gln Trp Glu Lys Pro
145 150 155 160

Lys Glu Trp Leu Glu Arg Glu Gln Arg Gln Lys Glu Ala Asn Lys Met
165 170 175

Ala Val Asn Ser Phe Pro Lys Asp Arg Asp Tyr Arg Arg Glu Val Met
180 185 190

Gln Ala Thr Ala Thr Ser Gly Phe Ala Ser Gly Lys Ser Thr Ser Gly
195 200 205

Asp Lys Pro Val Ser His Ser Cys Thr Thr Pro Ser Thr Ser Ser Ala
210 215 220

Ser Gly Leu Asn Pro Thr Ser Ala Pro Pro Thr Ser Ala Ser Ala Val
225 230 235 240

Pro Val Ser Pro Val Pro Gln Ser Pro Ile Pro Pro Leu Leu Gln Asp
245 250 255

Pro Asn Leu Leu Arg Gln Leu Leu Pro Ala Leu Gln Ala Thr Leu Gln
260 265 270

Leu Asn Asn Ser Asn Val Asp Ile Ser Lys Ile Asn Glu Val Leu Thr
275 280 285

Ala Ala Val Thr Gln Ala Ser Leu Gln Ser Ile Ile His Lys Phe Leu
290 295 300

Thr Ala Gly Pro Ser Ala Phe Asn Ile Thr Ser Leu Ile Ser Gln Ala
305 310 315 320

Ala Gln Leu Ser Thr Gln Ala Gln Pro Ser Asn Gln Ser Pro Met Ser
325 330 335

Leu Thr Ser Asp Ala Ser Ser Pro Arg Ser Tyr Val Ser Pro Arg Ile
340 345 350

Ser Thr Pro Gln Thr Asn Thr Val Pro Ile Lys Pro Leu Ile Ser Thr
355 360 365

Pro Pro Val Ser Ser Gln Pro Lys Val Ser Thr Pro Val Val Lys Gln
370 375 380

Gly Pro Val Ser Gln Ser Ala Thr Gln Gln Pro Val Thr Ala Asp Lys
385 390 395 400

Gln Gln Gly His Glu Pro Val Ser Pro Arg Ser Leu Gln Arg Ser Ser

405										410					415				
Gln	Arg	Ser	Pro	Ser	Pro	Gly	Pro	Asn	His	Thr	Ser	Asn	Ser	Ser	Asn				
			420					425					430						
Ala	Ser	Asn	Ala	Thr	Val	Val	Pro	Gln	Asn	Ser	Ser	Ala	Arg	Ser	Thr				
		435					440					445							
Cys	Ser	Leu	Thr	Pro	Ala	Leu	Ala	Ala	His	Phe	Ser	Glu	Asn	Leu	Ile				
		450				455					460								
Lys	His	Val	Gln	Gly	Trp	Pro	Ala	Asp	His	Ala	Glu	Lys	Gln	Ala	Ser				
465					470					475					480				
Arg	Leu	Arg	Glu	Glu	Ala	His	Asn	Met	Gly	Thr	Ile	His	Met	Ser	Glu				
				485					490					495					
Ile	Cys	Thr	Glu	Leu	Lys	Asn	Leu	Arg	Ser	Leu	Val	Arg	Val	Cys	Glu				
			500					505					510						
Ile	Gln	Ala	Thr	Leu	Arg	Glu	Gln	Arg	Ile	Leu	Phe	Leu	Arg	Gln	Gln				
		515					520					525							
Ile	Lys	Glu	Leu	Glu	Lys	Leu	Lys	Asn	Gln	Asn	Ser	Phe	Met	Val					
		530				535					540								

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

CAGTGGAGTC TGTACTGGCT GCGGGGGACC CTGCTCATTT GAAAATCTGA CATCAGCTGG	60
GCAGTCGCCC CCCTCCTCCT TTCCTCCCTC TACTCTGACA CAGCACTTAG CACCTGAATC	120
TTCGTTTCTC TCCCAGGGAC CCTCCATTTT CCATATCCAG GAAAATGTGA TGCGCCACAG	180
GTATCAGCGT CTGGATCGCC ACTTCACGTT TTAGCCACAA GTGACTCAGT GGAAGATCCA	240
GAGTCAACAG AGGCTCGTCA GGAAGATGTC TACAGAAAAG GTAGACCAAA AGGAGGAAGC	300
TGGGGAAAAA GAGGTGTGCG GAGACCAGAT CAARGGACCG GACAAAGAGG AGGAACCACC	360
AGCTGCTGCA TCCCATGGCC AGGGGTGGCG TCCAGGTGGC AGAGCAGCTA GGAACGCAAG	420
GCCTGAACCT GGGGCCAGAC ACCCTGCTCT CCCGGCCATG GTCAACGACC CTCCAGTACC	480
TGCCTTACTG TGGGCCCAGG AGGTGGGCCA AGTCTTGGCA GGCCGTGCCC GCAGGCTGCT	540

GCTGCAGTTT GGGGTGCTCT TCTGCACCAT CCTCCTTTTG CTCTGGGTGT CTGTCTTCCT	600
CTATGGCTCC TTCTACTATT CCTATATGCC GACAGTCAGC CACCTCAGCC CTGTGCATTT	660
CTACTACAGG ACCGACTGTG ATTCCTCCAC CACCTCACTC TGCTCCTTCC CTGTTGCCAA	720
TGTCTCGCTG ACTAAGGGTG GACGTGATCG GGTGCTGATG TATGGACAGC CGTATCGTGT	780
TACCTTAGAG CTTGAGCTGC CAGAGTCCCC TGTGAATCAA GATTTGGGCA TGTTCCTGGT	840
CACCATTTC TGCTACACCA GAGGTGGCCG AATCATCTCC ACTTCTTCGC GTTCGGTGAT	900
GCTGCATTAC CGCTCAGACC TGCTCCAGAT GCTGGACACA CTGGTCTTCT CTAGCCTCCT	960
GCTATTTGGC TTTGCAGAGC AGAAGCAGCT GCTGGAGGTG GAACTCTACG CAGACTATAG	1020
AGAGAACTCG TACGTGCCGA CCACTGGAGC GATCATTGAG ATCCACAGCA AGCGCATCCA	1080
GCTGTATGGA GCCTACCTCC GCATCCACGC GCACTTCACT GGGCTCAGAT ACCTGCTATA	1140
CAACTTCCCG ATGACCTGCG CCTTCATAGG TGTGCCAGC AACTTCACCT TCCTCAGCGT	1200
CATCGTGCTC TTCAGCTACA TGCAGTGGGT GTGGGGGGGC ATCTGGCCCC GACACCGCTT	1260
CTCTTTGCAG GTTAACATCC GAAAAAGAGA CAATTCCCGG AAGGAAGTCC AACGAAGGAT	1320
CTCTGCTCAT CAGCCAGGGC CTGAAGGCCA GGAGGAGTCA ACTCCGCAAT CAGATGTTAC	1380
AGAGGATGGT GAGAGCCCTG AAGATCCCTC AGGGACAGAG GGTCAGCTGT CCGAGGAGGA	1440
GAAACCAGAT CAGCAGCCCC TGAGCGGAGA AGAGGAGCTA GAGCCTGAGG CCAGTGATGG	1500
TTCAGGCTCC TGGGAAGATG CAGCTTTGCT GACGGAGGCC AACCTGCCTG CTCCTGCTCC	1560
TGCTTCTGCT TCTGCCCCTG TCCTAGAGAC TCTGGGCAGC TCTGAACCTG CTGGGGGTGC	1620
TCTCCGACAG CGCCCCACCT GCTCTAGTTC CTGAAGAAAA GGGGCAGACT CCTCACATTC	1680
CAGCACTTTC CCACCTGACT CCTCTCCCCT CGTTTTTCCT TCAATAAACT ATTTTGTGTC	1740
AAAAAAAAAA AAAAA	1755

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Met Ser Thr Glu Lys Val Asp Gln Lys Glu Glu Ala Gly Glu Lys Glu
1 5 10 15

Val Cys Gly Asp Gln Ile Lys Gly Pro Asp Lys Glu Glu Glu Pro Pro
20 25 30

Ala Ala Ala Ser His Gly Gln Gly Trp Arg Pro Gly Gly Arg Ala Ala
35 40 45

Arg Asn Ala Arg Pro Glu Pro Gly Ala Arg His Pro Ala Leu Pro Ala
50 55 60

Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val
65 70 75 80

Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly
85 90 95

Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val Phe Leu
100 105 110

Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
115 120 125

Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
130 135 140

Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
145 150 155 160

Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
165 170 175

Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
180 185 190

Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser
195 200 205

Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
210 215 220

Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
225 230 235 240

Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr
245 250 255

Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys Arg Ile Gln
260 265 270

Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr Gly Leu Arg
275 280 285

Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile Gly Val Ala
290 295 300

Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser Tyr Met Gln
305 310 315 320

Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser Leu Gln Val
325 330 335

Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln Arg Arg Ile
340 345 350

Ser Ala His Gln Pro Gly Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln
355 360 365

Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr
370 375 380

Glu Gly Gln Leu Ser Glu Glu Glu Lys Pro Asp Gln Gln Pro Leu Ser
385 390 395 400

Gly Glu Glu Glu Leu Glu Pro Glu Ala Ser Asp Gly Ser Gly Ser Trp
405 410 415

Glu Asp Ala Ala Leu Leu Thr Glu Ala Asn Leu Pro Ala Pro Ala Pro
420 425 430

Ala Ser Ala Ser Ala Pro Val Leu Glu Thr Leu Gly Ser Ser Glu Pro
435 440 445

Ala Gly Gly Ala Leu Arg Gln Arg Pro Thr Cys Ser Ser Ser
450 455 460

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GGAATAGAGG ATTTCAAAAA GCATGCGTTT TTTGAAGGTC TAAATTGGGA AAATATACGA	60
AACCTAGAAG CACCTTATAT TCCTGATGTG AGCAGTCCCT CTGACACATC CAACTTCGAC	120
GTGGATGACG ACGTGCTGAG AAACACGGAA ATATTACCTC CTGGTTCTCA CACAGGCTTT	180
TCTGGATTAC ATTTGCCATT CATTGGTTTT ACATTCACAA CGGAAAGCTG TTTTCTGAT	240
CGAGGCTCTC TGAAGAGCAT AATGCAGTCC AACACATTAA CCAAAGATGA GGATGTGCAG	300
CGGGACCTGG AGCACAGCCT GCAGATGGAA GCTTACGAGA GGAGGATTCTG GAGGCTGGAA	360
CAGGAGAAGC TGGAGCTGAG CAGGAAGCTG CAAGAGTCCA CCCAGACCGT GCAGTCCCTC	420

CACGGCTCAT	CTCGGGCCCT	CAGCAATTCA	AACCGAGATA	AAGAAATCAA	AAAGCTAAAT	480
GAAGAAATCG	AACGCTTGAA	GAATAAAATA	GCAGATTCAA	ACAGGCTGGA	GCGACAGCTT	540
GAGGACACAG	TGGCGCTTCG	CCAAGAGCGT	GAGGACTCCA	CGCAGCGGCT	GCGGGGGCTG	600
GAGAAGCAGC	ACCGCGTGGT	CCGGCAGGAG	AAGGAGGAGC	TGCACAAGCA	ACTGGTTGAA	660
GCCTCAGAGC	GGTTGAAATC	CCAGGCCAAG	GAACTCAAAG	ATGCCCATCA	GCAGCGAAAAG	720
CTGGCCCTGC	AGGAGTTCTC	GGAGCTGAAC	GAGCGCATGG	CAGAGCTCCG	TGCCCAGAAG	780
CAGAAGGTGT	CCCGGCAGCT	GCGAGACAAG	GAGGAGGAGA	TGGAGGTGGC	CACGCAGAAG	840
GTGGACGCCA	TGCGGCAGGA	AATGCGGAGA	GCTGAGAAGC	TCAGGAAAGA	GCTGGAAGCT	900
CAGCTTGATG	ATGCTGTTGC	TGAGGCCTCC	AAGGAGCGCA	AGCTTCGTGA	GCACAGCGAG	960
AACTTCTGCA	AGCAAATGGA	AAGCGAGCTG	GAGGCCCTCA	AGGTGAAGCA	AGGAGGCCCG	1020
GGAGCGGGTG	CCACCTTAGA	GCACCAGCAA	GAGATTTCCT	AAATCAAATC	CGAGCTGGAG	1080
AAGAAAGTCT	TATTTTATGA	AGAGGAATTG	GTCAGACGTG	AGGCCTCCCA	TGTGCTAGAA	1140
GTGAAAAATG	TGAAGAAGGA	GGTGCATGAT	TCAGAAAGCC	ACCAGCTGGC	CCTGCAGAAA	1200
GAAATCTTGA	TGTTAAAAGA	TAAGTTAGAA	AAGTCAAAGC	GAGAACGGCA	TAACGAGATG	1260
GAGGAGGCAG	TAGGTACAAT	AAAAGATAAA	TACGAACGAG	AAAGAGCGAT	GCTGTTTGAT	1320
GAAAACAAGA	AGCTAACTGC	TGAAAATGAA	AAGCTCTGTT	CCTTTGTGGA	TAAACTCACA	1380
GCTCAAAAATA	GACAGCTGGA	GGATGAGCTG	CAGGATCTGG	CAGCCAAGAA	GGAGTCAGTG	1440
GCCCACTGGG	AAGCTCAGAT	TGCGGAAATC	ATTCACTGGG	TCAGTGACGA	GAAAGATGCC	1500
CGGGGTTACC	TTCAAGCTCT	TGCTTCCAAG	ATGACCGAAG	AGCTCGAGGC	TTTGAGGAGT	1560
TCTAGTCTGG	GGTCAAGAAC	ACTGGACCCG	CTGTGGAAGG	TGCGCCGCAG	CCAGAAGCTG	1620
GACATGTCCG	CGCGGCTGGA	GCTGCAGTCG	GCCCTGGAGG	CGGAGATCCG	GGCCAAGCAG	1680
CTTGTCAGG	AGGAGCTCAG	GAAGGTCAAG	GACGCCAACC	TCACCTTGGA	AAGCAAACYA	1740
AWGGATTCCG	AAGCCAAAAA	CAGAGAATTA	TTAGAAGAAA	TGGAAATTTT	GAAGAAAAAG	1800
ATGGAAGAAA	AATTCAGAGC	AGATACTGGG	CTCAAACCTC	CAGATTTTCA	GGATTCCATT	1860
TTTGAGTATT	TCAACACTGC	TCCTCTTGCA	CATGACCCTGA	CATTTAGAAC	CAGCTCAGCT	1920
AGTGAGCAAG	AAACACAAGC	TCCGAAGCCA	GAAGCGTCCC	CGTCGATGTC	TGTGGCTGCA	1980
TCAGAGCAGC	AGGAGGACAT	GGCTCGGCCC	CCGCAGAGGC	CATCCGCTGT	GCCGTTGCCC	2040
ACCACGCAGG	CCCTGGCTCT	GGCTGGACCG	AAGCCAAAAG	CTCACCAGTT	CAGCATCAAG	2100

TCCTTCTCCA GCCCTACTCA GTGCAGCCAC TGCACCTCCC TGATGGTTGG GCTGATCCGG 2160
CAGGGCTACG CCTGCGAGGT GTGTTCTTTT GCTTGCCACG TGTCTGCAA AGACGGTGCC 2220
CCCCAGGTGT GCCCAATACC TCCCAGACAG TCCAAGAGGC CTCTGGGCGT GGACGTGCAG 2280
CGAGGCATCG GAACAGCCTA CAAAGGCCAT GTCAAGGTCC CAAAGCCCAC GGGGGTGAAG 2340
AAGGGATGGC AGCGCGCATA TGCAGTCGTC TGTGACTGCA AGCTCTTCCT GTATGATCTG 2400
CCTGAAGGAA AATCCACCCA GCCTGGTGTC ATTGCGAGCC AAGTCTTGGA TCTCAGAGAT 2460
GACGAGTTTT CCGTGAGCTC AGTCCTGGCC TCAGATGTCA TTCATGCTAC ACGCCGAGAT 2520
ATTCCATGTA TATTCAGGT GACGGCCTCT CTCTTAGGTG CACCTTCTAA GACCAGCTCG 2580
CTGCTCATTC TGACAGAAAA TGAGAATGAA AAGAGGAAGT GGGTTGGGAT TCTAGAAGGA 2640
CTCCAGTCCA TCCTTCATAA AAACCGGCTG AGGAATCAGG TCGTGCATGT TCCCTTGGA 2700
GCCTACGACA GCTCGCTGCC TCTCATCAAG GCCATCCTGA CAGCTGCCAT CGTGGATGCA 2760
GACAGGATTG CAGTCGGCCT AGAAGAAGGG CTCTATGTCA TAGAGGTCAC CCGAGATGTG 2820
ATCGTCCGTG CCGCTGACTG TAAGAAGGTA CACCAGATCG AGCTTGCTCC CAGGGAGAAG 2880
ATCGTAATCC TCCTCTGTGG CCGGAACCAC CATGTGCACC TCTATCCGTG GTCGTCCCTT 2940
GATGGAGCGG AAGGCAGCTT TGACATCAAG CTTCCGAAA CCAAAGGCTG CCAGCTCATG 3000
GCCACGGCCA CACTCAAGAG GARCTCTGGC ACCTGCCTGT TTGTGGCCGT GAAACGGCTG 3060
ATCCTTTGCT ATGAGATCCA GAAAATAAAG CCATATTGAA TGATAAAAAA AAAAAAAAAA 3120
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3180
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 3213

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Met Gln Ser Asn Thr Leu Thr Lys Asp Glu Asp Val Gln Arg Asp Leu
1 5 10 15
Glu His Ser Leu Gln Met Glu Ala Tyr Glu Arg Arg Ile Arg Arg Leu
20 25 30

Glu Gln Glu Lys Leu Glu Leu Ser Arg Lys Leu Gln Glu Ser Thr Gln
 35 40 45
 Thr Val Gln Ser Leu His Gly Ser Ser Arg Ala Leu Ser Asn Ser Asn
 50 55 60
 Arg Asp Lys Glu Ile Lys Lys Leu Asn Glu Glu Ile Glu Arg Leu Lys
 65 70 75 80
 Asn Lys Ile Ala Asp Ser Asn Arg Leu Glu Arg Gln Leu Glu Asp Thr
 85 90 95
 Val Ala Leu Arg Gln Glu Arg Glu Asp Ser Thr Gln Arg Leu Arg Gly
 100 105 110
 Leu Glu Lys Gln His Arg Val Val Arg Gln Glu Lys Glu Glu Leu His
 115 120 125
 Lys Gln Leu Val Glu Ala Ser Glu Arg Leu Lys Ser Gln Ala Lys Glu
 130 135 140
 Leu Lys Asp Ala His Gln Gln Arg Lys Leu Ala Leu Gln Glu Phe Ser
 145 150 155 160
 Glu Leu Asn Glu Arg Met Ala Glu Leu Arg Ala Gln Lys Gln Lys Val
 165 170 175
 Ser Arg Gln Leu Arg Asp Lys Glu Glu Glu Met Glu Val Ala Thr Gln
 180 185 190
 Lys Val Asp Ala Met Arg Gln Glu Met Arg Arg Ala Glu Lys Leu Arg
 195 200 205
 Lys Glu Leu Glu Ala Gln Leu Asp Asp Ala Val Ala Glu Ala Ser Lys
 210 215 220
 Glu Arg Lys Leu Arg Glu His Ser Glu Asn Phe Cys Lys Gln Met Glu
 225 230 235 240
 Ser Glu Leu Glu Ala Leu Lys Val Lys Gln Gly Gly Arg Gly Ala Gly
 245 250 255
 Ala Thr Leu Glu His Gln Gln Glu Ile Ser Lys Ile Lys Ser Glu Leu
 260 265 270
 Glu Lys Lys Val Leu Phe Tyr Glu Glu Glu Leu Val Arg Arg Glu Ala
 275 280 285
 Ser His Val Leu Glu Val Lys Asn Val Lys Lys Glu Val His Asp Ser
 290 295 300
 Glu Ser His Gln Leu Ala Leu Gln Lys Glu Ile Leu Met Leu Lys Asp
 305 310 315 320
 Lys Leu Glu Lys Ser Lys Arg Glu Arg His Asn Glu Met Glu Glu Ala
 325 330 335

Val Gly Thr Ile Lys Asp Lys Tyr Glu Arg Glu Arg Ala Met Leu Phe
340 345 350

Asp Glu Asn Lys Lys Leu Thr Ala Glu Asn Glu Lys Leu Cys Ser Phe
355 360 365

Val Asp Lys Leu Thr Ala Gln Asn Arg Gln Leu Glu Asp Glu Leu Gln
370 375 380

Asp Leu Ala Ala Lys Lys Glu Ser Val Ala His Trp Glu Ala Gln Ile
385 390 395 400

Ala Glu Ile Ile Gln Trp Val Ser Asp Glu Lys Asp Ala Arg Gly Tyr
405 410 415

Leu Gln Ala Leu Ala Ser Lys Met Thr Glu Glu Leu Glu Ala Leu Arg
420 425 430

Ser Ser Ser Leu Gly Ser Arg Thr Leu Asp Pro Leu Trp Lys Val Arg
435 440 445

Arg Ser Gln Lys Leu Asp Met Ser Ala Arg Leu Glu Leu Gln Ser Ala
450 455 460

Leu Glu Ala Glu Ile Arg Ala Lys Gln Leu Val Gln Glu Glu Leu Arg
465 470 475 480

Lys Val Lys Asp Ala Asn Leu Thr Leu Glu Ser Lys Xaa Xaa Asp Ser
485 490 495

Glu Ala Lys Asn Arg Glu Leu Leu Glu Glu Met Glu Ile Leu Lys Lys
500 505 510

Lys Met Glu Glu Lys Phe Arg Ala Asp Thr Gly Leu Lys Leu Pro Asp
515 520 525

Phe Gln Asp Ser Ile Phe Glu Tyr Phe Asn Thr Ala Pro Leu Ala His
530 535 540

Asp Leu Thr Phe Arg Thr Ser Ser Ala Ser Glu Gln Glu Thr Gln Ala
545 550 555 560

Pro Lys Pro Glu Ala Ser Pro Ser Met Ser Val Ala Ala Ser Glu Gln
565 570 575

Gln Glu Asp Met Ala Arg Pro Pro Gln Arg Pro Ser Ala Val Pro Leu
580 585 590

Pro Thr Thr Gln Ala Leu Ala Leu Ala Gly Pro Lys Pro Lys Ala His
595 600 605

Gln Phe Ser Ile Lys Ser Phe Ser Ser Pro Thr Gln Cys Ser His Cys
610 615 620

Thr Ser Leu Met Val Gly Leu Ile Arg Gln Gly Tyr Ala Cys Glu Val
625 630 635 640

Cys Ser Phe Ala Cys His Val Ser Cys Lys Asp Gly Ala Pro Gln Val
645 650 655

Cys Pro Ile Pro Pro Glu Gln Ser Lys Arg Pro Leu Gly Val Asp Val
660 665 670

Gln Arg Gly Ile Gly Thr Ala Tyr Lys Gly His Val Lys Val Pro Lys
675 680 685

Pro Thr Gly Val Lys Lys Gly Trp Gln Arg Ala Tyr Ala Val Val Cys
690 695 700

Asp Cys Lys Leu Phe Leu Tyr Asp Leu Pro Glu Gly Lys Ser Thr Gln
705 710 715 720

Pro Gly Val Ile Ala Ser Gln Val Leu Asp Leu Arg Asp Asp Glu Phe
725 730 735

Ser Val Ser Ser Val Leu Ala Ser Asp Val Ile His Ala Thr Arg Arg
740 745 750

Asp Ile Pro Cys Ile Phe Arg Val Thr Ala Ser Leu Leu Gly Ala Pro
755 760 765

Ser Lys Thr Ser Ser Leu Leu Ile Leu Thr Glu Asn Glu Asn Glu Lys
770 775 780

Arg Lys Trp Val Gly Ile Leu Glu Gly Leu Gln Ser Ile Leu His Lys
785 790 795 800

Asn Arg Leu Arg Asn Gln Val Val His Val Pro Leu Glu Ala Tyr Asp
805 810 815

Ser Ser Leu Pro Leu Ile Lys Ala Ile Leu Thr Ala Ala Ile Val Asp
820 825 830

Ala Asp Arg Ile Ala Val Gly Leu Glu Glu Gly Leu Tyr Val Ile Glu
835 840 845

Val Thr Arg Asp Val Ile Val Arg Ala Ala Asp Cys Lys Lys Val His
850 855 860

Gln Ile Glu Leu Ala Pro Arg Glu Lys Ile Val Ile Leu Leu Cys Gly
865 870 875 880

Arg Asn His His Val His Leu Tyr Pro Trp Ser Ser Leu Asp Gly Ala
885 890 895

Glu Gly Ser Phe Asp Ile Lys Leu Pro Glu Thr Lys Gly Cys Gln Leu
900 905 910

Met Ala Thr Ala Thr Leu Lys Arg Xaa Ser Gly Thr Cys Leu Phe Val
915 920 925

Ala Val Lys Arg Leu Ile Leu Cys Tyr Glu Ile Gln Lys Ile Lys Pro
930 935 940

Tyr
945

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGGGCACTT AATCCCAATG AACTGTATGC TTAAAAATAA TTTAAATGAT AAACTTTGTG	60
TTATGTATAC TTTACCACAA TAAGAAAAAG TATTTTAGTA CTAGTGGTAA ATAGTTTTTA	120
TTTAATAGAC TTATATTTTA AAGCTTAAAA ATAATTTAGC TTCTAGAGTA TTACGTTTTT	180
CTTCATGGGA ACTTCAAAAA GCAAGTCACT AAATCCAAGA ATTTTAAAGA AAAAACCCAA	240
ATACATGATT TATGCTGCAT CTGGTATAGA TTTTAAAAAG ACTAGTCAAT CTAAGCTCTA	300
AACTATTAAA TGACAAACCA TTCATATGT CATTGCATAT TCCTATGTAC CACATTCTCA	360
TATTTCTGTT ATGGGCATGA AGGGGTGTTT GATGCTTCCA TGCCATAATA ACCATGACTA	420
TCACAACCAT TGAAATAAAG GTTCTTGCGT TATTTTCAGG ATGGTCCCAG AAATTTAAAT	480
TAATCTCTCA TCCATTGGCT TTTGCTACTT TAGGTTAATA TTAAAATATA ACATACATTT	540
TTGGGGTTTA TGCTGTTAGC TCCAAACCAA AAGATTTTGG AAATTTATTT TGGAAATTTT	600
GTGTTTAGAA TATGAATAAA TCTGCTTATT CAGAAAAATT AAACCTTGAT AACTTGGGAC	660
CTCCTATTCC TGTATGTTCT CTGACATACA TTGAGGGATT TGGCTCTCTT TTGTTTATTT	720
GTTTTACTAG TCAGACATTC CTTTGGCTGC CCATACTTAA TTCTGTTGGG TGTTTCCGCC	780
CCCGCCCTCA GCTTCTGCAG CTACTCTGAT CAACATCCGC AATGCCAGGA AACACTTTGA	840
AAAGCTGGAA AGAGTGGATG GACCAAAGCA GTGTCTTCTC ATGCGCTAAA CATTGATGAA	900
TATTGTTTCA CACAAAAATT AAAAGTTTCC TAATTAATGT TGTATTCATA TATGTAGGCT	960
CTGAAATGTT GTGATGCTTA TTGCTTCTGT ATTTCTTCTC TACTCCCTAG TCTTAATGTT	1020
TAACCTTGAA TGCTATTAAC TTAAATAGCC ATTGAGGAGT TAGAAGATGA ATTGTTCATG	1080
AAGTCGGTGT TACATAAAAG TAGGTGATAT GTAAGTTTTC TGATAACAAG GTTCTAATAG	1140
TGTTTAAATG TACTGGTAAC CTGGTTCCAA TAGTTGTGTT TGCCCAAGCC TTTCTCGGCA	1200
TCATCTTGTA TTCCTTATCA GATAGTAAGT AACCTGTAAG TTTGGAGTAT TACTGTTTTT	1260
TCAGCATGCA TTAAAAATAT TCCTTAACTT CAATTGTAAA AAAAAAAAAA AAAAA	1315

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

Met Asn Lys Ser Ala Tyr Ser Glu Lys Leu Asn Leu Asp Asn Leu Gly
1           5           10           15

Pro Pro Ile Pro Val Cys Ser Leu Thr Tyr Ile Glu Gly Phe Gly Ser
          20           25           30

Leu Leu Phe Ile Cys Phe Thr Ser Gln Thr Phe Leu Trp Leu Pro Ile
          35           40           45

Leu Asn Ser Val Gly Cys Phe Arg Pro Arg Pro Gln Leu Leu Gln Leu
          50           55           60

Leu
65
  
```

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

TAGGCCATGA AGGCCGAATC GGCCTTCATG GCCTACGCTT ACACAATACC CACCATGTCC      60
CAGGCTGGTG CTCAGGAAGC CCCTATCAAG AAGAAGCGCC CCCCTGTGAA GGAGGAGGAC      120
CTGAAGGGGG CCCGAGGAAA CCTGACCAAG AACCAGGAAA TCAAGTCCAA GACCTACCAG      180
GTCATGCGAG AGTGTGAGCA AGCTGGCTCG GCCGCCCCGT CGGTGTTTCAG CCGCACCCGC      240
ACAGGTACCG AGACTGTCTT TGAGAAGCCC AAAGCCGGAC CCACCAAGAG TGTCTTCGGC      300
TGAGAAGTGT GCGCCACTCC CCTTGCTGCC CGAATGCTCG GAAACAGGAG CCTTACCCAG      360
GAACTCTTTT TTATGCCAGA ACGCTTCCTC TCCCCTGCTG TCTCTGGGGC TGCCACCCTC      420
  
```

CCCCACAGTC CAGGCCCTTC AGCCAAGGGC TCTGCACCAG CACCTTGGA GCACCAATAA 480
AGAGGATGCC CACGTGGCCC CAGCAAAAAA AAAAAAAAAA 519

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Met	Lys	Ala	Glu	Ser	Ala	Phe	Met	Ala	Tyr	Ala	Tyr	Thr	Ile	Pro	Thr	
1				5					10					15		
Met	Ser	Gln	Ala	Gly	Ala	Gln	Glu	Ala	Pro	Ile	Lys	Lys	Lys	Arg	Pro	
			20					25						30		
Pro	Val	Lys	Glu	Glu	Asp	Leu	Lys	Gly	Ala	Arg	Gly	Asn	Leu	Thr	Lys	
			35				40					45				
Asn	Gln	Glu	Ile	Lys	Ser	Lys	Thr	Tyr	Gln	Val	Met	Arg	Glu	Cys	Glu	
			50			55					60					
Gln	Ala	Gly	Ser	Ala	Ala	Pro	Ser	Val	Phe	Ser	Arg	Thr	Arg	Thr	Gly	
			65			70				75					80	
Thr	Glu	Thr	Val	Phe	Glu	Lys	Pro	Lys	Ala	Gly	Pro	Thr	Lys	Ser	Val	
						85				90				95		
Phe	Gly															

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GACGGCGACC	AAACCCAGCT	AGGTCAGACG	AGAAAGATAA	AAACTCTCCA	GATGTCTTCC	60
AGTAATGTCTG	AAGTTTTTAT	CCCAGTGTCA	CAAGGAAACA	CCAATGGCTT	CCCCGCGACA	120
GCTTCCAATG	ACCTGAAGGC	ATTTACTGAA	GGAGCTGTGT	TAAGTTTTC	TAACATCTGC	180

TATCGAGTAA AACTGAAGAG TGGCTTTCTA CCTTGTCGAA AACCAGTTGA GAAAGAAATA 240
TTATCGAATA TCAATGGGAT CATGAAACCT GGTCTCAACG CCATCCTGGG ACCCACAGGT 300
GGARGCAAAT CTTTCGTTATT AGATGTCTTA GCTGCAAGGA AAGATCCAAG TGGATTATCT 360
GGAGATGTTT TGATAAATGG AGCACCGCGA CCTGCCAATT TCAAATGTAA TTCAGGTTAC 420
GTGGTACAAG TTGGAACCTCA GTTTATCCGT GGTGTGTCTG GAGGAGAAAG AAAAAGGACT 480
AGTATAGGAA TGGAGCTTAT CACTGATCCT TCCATCTTGT TCTTGGATGA GCCTACAACCT 540
GGCTTAGACT CAAGCACAGC AAATGCTGTC CTTTTGCTCC TGAAAAGGAT GTCTAAGCAG 600
GGACGAACAA TCATCTTCTC CATTTCATCAG CCTCGATATT CCATCTTCAA GTTGTTTGAT 660
AGCCTCACCT TATTGGCCTC AGGAAGACTT ATGTTCCACG GGCCTGCTCA GGAGGCCTTG 720
GGATACTTTG AATCAGCTGG TTATCACTGT GAGGCCTATA ATAACCCTGC AGACTTCTTC 780
TTGGACATCA TTAATGGAGA TTCCACTGCT GTGGCATTAA ACAGAGAAGA AGACTTTAAA 840
GCCACAGAGA TCATAGAGCC TTCCAAGCAG GATAAGCCAC TCATAGAAAA ATTAGCGGAG 900
ATTTATGTCA ACTCCTCCTT CTACAAAGAG ACAAAGCTG AATTACATCA ACTTTCCGGG 960
GGTGAGAAGA AGAAGAAGAT CACAGTCTTC AAGGAGATCA GCTACACCAC CTCCTTCTGT 1020
CATCAACTCA GATGGGTTTC CAAGCGTTCA TTCAAAAACCT TGCTGGGTAA TCCCCAGGCC 1080
TCTATAGCTC AGATCATTGT CACAGTCGTA CTGGGACTGG TTATAGGTGC CATTTACTTT 1140
GGGCTAAAAA ATGATTCTAC TGGAATCCAG AACAGAGCTG GGGTCTCTCTT CTTCTGACG 1200
ACCAACCAGT GTTTCAGCAG TGTTTCAGCC GTGGAACCTT TTGTGGTAGA GAAGAAGCTC 1260
TTCATACATG AATACATCAG CGGATACTAC AGAGTGTCAT CTTATTTCTT TGGAAAACCTG 1320
TTATCTGATT TATTACCCAT GAGGATGTTA CCAAGTATTA TATTTACCTG TATAGTGATC 1380
TTCATGTTAG GATTGAAGCC AAAGGCAGAT GCCTTCTTCG TTATGATGTT TACCCTTATG 1440
ATGGTGGCTT ATTCAGCCAG TTCCATGGCA CTGGCCATAG CAGCAGGTCA GAGTGTGGTT 1500
TCTGTAGCAA CACTTCTCAT GACCATCTGT TTTGTGTTTA TGATGATTTT TTCAGGTCTG 1560
TTGGTCAATC TCACAACCAT TGCATCTTGG CTGTCATGGC TTCAGTACTT CAGCATTCCA 1620
CGATATGGAT TTACGGCTTT GCAGCATAAT GAATTTTGG GACAAAACCT CTGCCCAGGA 1680
CTCAATGCAA CAGGAAACAA TCCTTGTAAC TATGCAACAT GTACTGGCGA AGAATATTTG 1740
GTAAAGCAGG GCATCGATCT CTCACCCTGG GGCTTGTGGA AGAATCACGT GGCCTTGGCT 1800
TGTATGATTG TTATTTTCTT CACAATTGCC TACCTGAAAT TGTTATTTCT TAAAAAATAT 1860

TCTTAAATTT CCCCTTAATT CAGTATGATT TATCCTCACA TAAAAAAGAA GCACTTTGAT 1920
TGAAGTATTC AATCAAGTTT TTTTGGTTGT TTTCTGTTCC CTTGCCATCA CACTGTTGCA 1980
CAGCAGCAAT TGTTTTAAAG AGATACATTT TTAGAAATCA CAACAAACTG AATTAAACAT 2040
GAAAGAACCC AAGACATCAT GTATCGCATA TTAGTTAATC TCCTCAGACA GTAACCATGG 2100
GGAAGAAATC TGGTCTAATT TATTAATCTA AAAAAGGAGA ATTGAATTCT GGAAACTCCT 2160
GACAAGTTAT TACTGTCTCT GGCATTTGTT TCCTCATCTT TAAAATGAAT AGGTAGGTTA 2220
GTAGCCCTTC AGTCTTAATA CTTTATGATG CTATGGTTTG CCATTATTTA ATAAATGACA 2280
AATGTATTAA TGCTAAAAAA AAAAAAAAAA AGCGGCCTTC ATGGCCTAGA GATTTCAACT 2340
TAACTTGACC GCTCTGAGCT AAACCTAGCC CCAAACCCAC TCCACCTTAT TACCAGACAA 2400
CCTTAACCAA ACCATTTACC CAAATAAAGT ATAGGCGATA GAAATTGAAA CCTGGCGCAA 2460
TAGATATAGT ACCGCAAGGG AAAGATGAAA AATTATAACC AAGCATAATA TAGCAAGGAC 2520
TAACCCCTAT ACCTTCTGCA TAATGAATTA ACTAGAAATA ACTTTGCAAG GAGAGCCAAA 2580
GCTAAGACCC CCGAAACCAG ACGAGCTACC TAAGAACAGC TAAAAGAGCA CACCCGTCTA 2640
TGTAGCAAAA TAGTGGGAAG ATTTATAGGT AGAGGCGACA AACCTACCGA GCCTGGTGAT 2700
AGCTGGTTGT CCCAGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760
AAAAAAAAA AAAAAAAAAA AAAAAAAA 2788

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met Ser Ser Ser Asn Val Glu Val Phe Ile Pro Val Ser Gln Gly Asn
1 5 10 15
Thr Asn Gly Phe Pro Ala Thr Ala Ser Asn Asp Leu Lys Ala Phe Thr
20 25 30
Glu Gly Ala Val Leu Ser Phe His Asn Ile Cys Tyr Arg Val Lys Leu
35 40 45
Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
50 55 60

Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
65 70 75 80

Pro Thr Gly Gly Xaa Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
85 90 95

Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
100 105 110

Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Val Gly
115 120 125

Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys Arg Thr Ser
130 135 140

Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Phe Leu Asp Glu
145 150 155 160

Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val Leu Leu Leu
165 170 175

Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe Ser Ile His
180 185 190

Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu Thr Leu Leu
195 200 205

Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu Ala Leu Gly
210 215 220

Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn Asn Pro Ala
225 230 235 240

Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala Val Ala Leu
245 250 255

Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu Pro Ser Lys
260 265 270

Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr Val Asn Ser
275 280 285

Ser Phe Tyr Lys Glu Thr Lys Ala Glu Leu His Gln Leu Ser Gly Gly
290 295 300

Glu Lys Lys Lys Lys Ile Thr Val Phe Lys Glu Ile Ser Tyr Thr Thr
305 310 315 320

Ser Phe Cys His Gln Leu Arg Trp Val Ser Lys Arg Ser Phe Lys Asn
325 330 335

Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile Val Thr Val
340 345 350

Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu Lys Asn Asp
355 360 365

Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe Leu Thr Thr
370 375 380

Asn Gln Cys Phe Ser Ser Val Ser Ala Val Glu Leu Phe Val Val Glu
385 390 395 400

Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr Arg Val Ser
405 410 415

Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro Met Arg Met
420 425 430

Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met Leu Gly Leu
435 440 445

Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr Leu Met Met
450 455 460

Val Ala Tyr Ser Ala Ser Ser Met Ala Leu Ala Ile Ala Ala Gly Gln
465 470 475 480

Ser Val Val Ser Val Ala Thr Leu Leu Met Thr Ile Cys Phe Val Phe
485 490 495

Met Met Ile Phe Ser Gly Leu Leu Val Asn Leu Thr Thr Ile Ala Ser
500 505 510

Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr Gly Phe Thr
515 520 525

Ala Leu Gln His Asn Glu Phe Leu Gly Gln Asn Phe Cys Pro Gly Leu
530 535 540

Asn Ala Thr Gly Asn Asn Pro Cys Asn Tyr Ala Thr Cys Thr Gly Glu
545 550 555 560

Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp Gly Leu Trp
565 570 575

Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe Leu Thr Ile
580 585 590

Ala Tyr Leu Lys Leu Leu Phe Leu Lys Lys Tyr Ser
595 600

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2930 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CGACTTCCTC	GGCTGCGCGG	CGCTCGCGCG	GAGCTCCCCG	GCCGGCGGTG	CGTCCCCACG	60
GTCACCATGA	AAGACGACTT	CGCAGAGGAG	GAGGAGGTGC	AATCCTTCGG	TTACAAGCGG	120
TTTGGTATTC	AGGAAGGAAC	ACAATGTACC	AAATGTAAAA	ATAACTGGGC	ACTGAAGTTT	180
TCTATCATAT	TATTATACAT	TTTGTGTGCC	TTGCTAACAA	TCACAGTAGC	CATTTTGGGA	240
TATAAAGTTG	TAGAGAAAAT	GGACAATGTC	ACAGGTGGCA	TGGAACATC	TCGCCAAACC	300
TATGATGACA	AGCTCACAGC	AGTGGAAGT	GACCTGAAAA	AATTAGGTGA	CCAAACTGGG	360
AAGAAAGCTA	TCAGCACCAA	CTCAGAACTC	TCCACCTTCA	GATCAGACAT	TCTAGATCTC	420
CGTCAGCAAC	TTCGTGAGAT	TACAGAAAAA	ACCAGCAAGA	ACAAGGATAC	GCTGGAGAAG	480
TTACAGGCGA	GCGGGGATGC	TCTGGTGGAC	AGGCAGAGTC	AATTGAAAGA	AACTTTGGAG	540
AATAACTCTT	TCCTCATCAC	CACTGTAAAC	AAAACCCTCC	AGGCGTATAA	TGGCTATGTC	600
ACGAATCTGC	AGCAAGATAC	CAGCGTGCTC	CAGGGCAATC	TGCAGAACCA	AATGTATTCT	660
CATAATGTGG	TCATCATGAA	CTCAACAACC	TGAACCTGAC	CCAGGTGCAG	CAGAGGAACC	720
TCATCACGAA	TCTGCAGCGG	TCTGTGGATG	ACACAAGCCA	GGCTATCCAG	CGAATCAAGA	780
ACGACTTTCA	AAATCTGCAG	CAGGTTTTTC	TTCAAGCCAA	GAAGGACACG	GATTGGCTGA	840
AGGAGAAAGT	GCAGAGCTTG	CAGACGCTGG	CTGCCAACAA	CTCTGCGTTG	GCCAAAGCCA	900
ACAACGACAC	CCTGGAGGAT	ATGAACAGCC	AGCTCAACTC	ATTCACAGGT	CAGATGGAGA	960
ACATCACCAC	TATCTCTCAA	GCCAACGAGC	AGAACCTGAA	AGACCTGCAG	GACTTACACA	1020
AAGATGCAGA	GAATAGAACA	GCCATCAAGT	TCAACCAACT	GGAGGAACGC	TTCCAGCTCT	1080
TTGAGACGGA	TATTGTGAAC	ATCATTAGCA	ATATCAGTTA	CACAGCCCAC	CACCTGCGGA	1140
CGCTGACCAG	CAATCTAAAT	GAAGTCAGGA	CCACTTGCAC	AGATACCCTT	ACCAAACACA	1200
CAGATGATCT	GACCTCCTTG	AATAATACCC	TGGCCAACAT	CCGTTTGGAT	TCTGTTTCTC	1260
TCAGGATGCA	ACAAGATTTG	ATGAGGTCGA	GGTTAGACAC	TGAAGTAGCC	AACTTATCAG	1320
TGATTATGGA	AGAAATGAAG	CTAGTAGACT	CCAAGCATGG	TCAGCTCATC	AAGAATTTTA	1380
CAATACTACA	AGGTCCACCG	GGCCCCAGGG	GTCCAAGAGG	TGACAGAGGA	TCCCAGGGAC	1440
CCCCTGGCCC	AACTGGCAAC	AAGGGACAGA	AAGGAGAGAA	GGGGGAGCCT	GGACCACCTG	1500
GCCCTGCGGG	TGAGAGAGGC	CCAATTGGAC	CAGCTGGTCC	CCCCGAGAG	CGTGGCGGCA	1560
AAGGATCTAA	AGGCTCCCAG	GGCCCCAAAG	GCTCCCGTGG	TTCCCCTGGG	AAGCCCGGCC	1620
CTCAGGGCCC	CAGTGGGGAC	CCAGGCCCCC	CGGGCCCACC	AGGCAAAGAG	GGACTCCCCG	1680

GCCCTCAGGG CCCTCCTGGC TTCCAGGGAC TTCAGGGCAC CGTTGGGGAG CCTGGGGTGC	1740
CTGGACCTCG GGGACTGCCA GGCTTGCCTG GGGTACCAGG CATGCCAGGC CCCAAGGGCC	1800
CCCCCGGCCC TCCTGGCCCA TCAGGAGCGG TGGTGCCCTT GGCCCTGCAG AATGAGCCAA	1860
CCCCGGCACC GGAGGACAAT AGCTGCCCCG CACTACTGGAA GAACTTCACA GACAAATGCT	1920
ACTATTTTTC AGTTGAGAAA GAAATTTTTC AGGATGCAAA GCTTTTCTGT GAAGACAAGT	1980
CTTCACATCT TGTTTTCATA AACACTAGAG AGGAACAGCA ATGGATAAAA AAACAGATGG	2040
TAGGGAGAGA GAGCCACTGG ATCGGCCTCA CAGACTCAGA GCGTGAAAAAT GAATGGAAGT	2100
GGCTGGATGG GACATCTCCA GACTACAAAA ATTGGAAAGC TGGACAGCCG GATAACTGGG	2160
GTCATGGCCA TGGGCCAGGA GAAGACTGTG CTGGGTTGAT TTATGCTGGG CAGTGAACG	2220
ATTTCCAATG TGAAGACGTC AATAACTTCA TTTGCGAAAA AGACAGGGAG ACAGTACTGT	2280
CATCTGCATT ATAACGGACT GTGATGGGAT CACATGAGCA AATTTTCAGC TCTCAAAGGC	2340
AAAGGACACT CCTTTCTAAT TGCATCACCT TCTCATCAGA TTGAAAAAAAA AAAAGCACTG	2400
AAAGCCAATT ACTGAAAAAA AATTGACAGC TAGTGTTTTT TACCATCCGT CATTACCCAA	2460
AGACTTGGGA ACTAAAAATGT TCCCCAGGGT GATATGCTGA TTTTCATTGT GCACATGGAC	2520
TGAATCACAT AGATTCTCCT CCGTCAGTAA CCGTGCGATT ATACAAATTA TGTCTTCCAA	2580
AGTATGGAAC ACTCCAATCA GAAAAAGGTT ATCATTTGGT GTTGAGTTAT GGGAGAAGT	2640
TAAGCATATA CTGTGTAAAC AGTGCCATAC ATTTCTAAAA TCCAAGTGT AGGAAAAATA	2700
TGCAGACATA CAGATATATA GGCCAACTAT TAGTAATAAT ATGAAATATA CTAAAGAGC	2760
TTTTAAAACT TTGTATTTTT GTACAAAATA TTTGTCTTTT ACAATTTTTT TCCTTTTTTT	2820
TTTTTTGTCA TTTTACCGAC ATAATACATG GAGCCAAAGA AAACAATAAT GGTACTAATA	2880
AAAACCTCCTA GGGTTTCCTG TCAGATTTAA TTCTAAAAAA AAAAAAAAAA	2930

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Met Lys Asp Asp Phe Ala Glu Glu Glu Glu Val Gln Ser Phe Gly Tyr

1	5	10	15
Lys Arg Phe Gly Ile Gln Glu Gly Thr Gln Cys Thr Lys Cys Lys Asn			
20	25	30	
Asn Trp Ala Leu Lys Phe Ser Ile Ile Leu Leu Tyr Ile Leu Cys Ala			
35	40	45	
Leu Leu Thr Ile Thr Val Ala Ile Leu Gly Tyr Lys Val Val Glu Lys			
50	55	60	
Met Asp Asn Val Thr Gly Gly Met Glu Thr Ser Arg Gln Thr Tyr Asp			
65	70	75	80
Asp Lys Leu Thr Ala Val Glu Ser Asp Leu Lys Lys Leu Gly Asp Gln			
85	90	95	
Thr Gly Lys Lys Ala Ile Ser Thr Asn Ser Glu Leu Ser Thr Phe Arg			
100	105	110	
Ser Asp Ile Leu Asp Leu Arg Gln Gln Leu Arg Glu Ile Thr Glu Lys			
115	120	125	
Thr Ser Lys Asn Lys Asp Thr Leu Glu Lys Leu Gln Ala Ser Gly Asp			
130	135	140	
Ala Leu Val Asp Arg Gln Ser Gln Leu Lys Glu Thr Leu Glu Asn Asn			
145	150	155	160
Ser Phe Leu Ile Thr Thr Val Asn Lys Thr Leu Gln Ala Tyr Asn Gly			
165	170	175	
Tyr Val Thr Asn Leu Gln Gln Asp Thr Ser Val Leu Gln Gly Asn Leu			
180	185	190	
Gln Asn Gln Met Tyr Ser His Asn Val Val Ile Met Asn Ser Thr Thr			
195	200	205	

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1589 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

TCTATATATT TTTTCTAGGA AGGGGTGTTT TTCTTTCTGA TTAAATTCCTT TACATTTTTC	60
TCTTTCATAT GAAGTTGCAG ATAATGTTTT TCCTTCGGAT TTTTATTCTT TAAGATTTTT	120
AACCTGTGCA AGACTTTTTC AATGATACAA GTCAAGGAGG ATGAAGATCT TTTTCCACTT	180

CAGTCTTCAC	TTTGCTCCAG	CTATTGCTAA	GAAAGGCACA	AACAATGACA	GCATATTTAA	240
GGAAGAACCT	GGCCGGCTTG	GGTCACCGCT	GCTGTCTTTC	TTGGTTTTGC	GTCTACCTGG	300
GAGAGCCCAG	CTTTTAGGTT	CCCATTGAGG	GAAGCATGAG	AGAGGATTGT	TTGGGGGATG	360
CTGCCAGAGC	TTCCAGCTGA	CAGTCTCTGC	AGAGCGGCTG	CCAAGTGGCC	TGGTGGCCGT	420
ATGTTGGCAG	TTTTTGATGA	ATTGGGATTA	GGGAATGTTT	GTTTACTTGA	TAACCGAGTG	480
TCTACAAGGA	GAGGTGGCAG	CGTGAGGGAA	TAGTGCCACC	ATAATGAGGA	CACAGCCAGC	540
CATCTCTTCC	CTGCCACAGA	ACCCAGGCA	GTCCCCTTCA	GGCTACAGTT	TTCCATCTGG	600
ACCGAGGGAC	TGGCCGGTGC	AGCAGGAGGA	GCCGATCACC	CTCTGTGGGA	ACGAGGATGC	660
CCAGAAGTTC	CAGTTACTGT	GGCTCCATGG	TCCCCTTCTC	GATGCGCATC	TTGCACGCGG	720
AGCTTCAGCA	GTACCTGGGG	AACCCACAGG	AGTCGCTGGA	TAGACTGCAC	AAGGTGAAGA	780
CTGTCTGCAG	CAAGATCCTG	GCCAATTTGG	AGCAAGGCTT	AGCAGAAGAC	GGCGGCATGA	840
GCAGCGTGAC	TCAGGAGGGC	AGACAAGCCT	CTATCCGGCT	GTGGAGGTCA	CGTCTGGGCC	900
GGGTGATGTA	CTCCATGGCA	AACTGTCTGC	TCCTGATGAA	GGATTATGTG	CTGGCCGTGG	960
AGGCGTATCA	TTCGGTTATC	AAGTATTACC	CAGAGCAAGA	GCCCCAGCTG	CTCAGCGGCA	1020
TCGGCCGGAT	TTCCTGTCAG	ATTGGAGACA	TAAAAACAGC	TGAAAAGTAT	TTTCAAGACG	1080
TTGAGAAAGT	AACACAGAAA	TTAGATGGAC	TACAGGGTAA	AATCATGGTT	TTGATGAACA	1140
GCGCGTTCCT	TCACCTCGGG	CAGAATAACT	TTGCAGAAAGC	CCACAGGTTC	TTACACAGAGA	1200
TCTTAAGGAT	GGATCCAAGA	AACGCAGTGG	CCAACAACAA	CGCTGCCGTG	TGTCTGCTCT	1260
ACCTGGGCAA	GCTCAAGGAC	TCCCTGCGGC	AGCTGGAGGC	CATGGTCCAG	CAGGACCCCA	1320
GGCACTACCT	GCACGAGAGC	GTGCTCTTCA	ACCTGACCAC	CATGTACGAG	CTGGAGTCCT	1380
CACGGAGCAT	GCAGAAGAAA	CAGGCCCTGC	TGGAGGCTGT	CGCCGGCAAG	GAGGGGGACA	1440
GCTTCAACAC	ACAGTGCCTC	AAGCTGGCCT	AGCTGCCTCC	AACACACTAC	GTCAGAAGGA	1500
CCCGGGTCTT	TGAAACTGTG	TCTTGAAGCT	AATGTATTAA	TGTGACATGG	AGGAACTCAA	1560
TAAAACTCCT	GCTTCAAAAA	AAAAAAAAAA				1589

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Met	Pro	Arg	Ser	Ser	Ser	Tyr	Cys	Gly	Ser	Met	Val	Pro	Phe	Ser	Met	1	5	10	15
Arg	Ile	Leu	His	Ala	Glu	Leu	Gln	Gln	Tyr	Leu	Gly	Asn	Pro	Gln	Glu	20	25	30	
Ser	Leu	Asp	Arg	Leu	His	Lys	Val	Lys	Thr	Val	Cys	Ser	Lys	Ile	Leu	35	40	45	
Ala	Asn	Leu	Glu	Gln	Gly	Leu	Ala	Glu	Asp	Gly	Gly	Met	Ser	Ser	Val	50	55	60	
Thr	Gln	Glu	Gly	Arg	Gln	Ala	Ser	Ile	Arg	Leu	Trp	Arg	Ser	Arg	Leu	65	70	75	80
Gly	Arg	Val	Met	Tyr	Ser	Met	Ala	Asn	Cys	Leu	Leu	Leu	Met	Lys	Asp	85	90	95	
Tyr	Val	Leu	Ala	Val	Glu	Ala	Tyr	His	Ser	Val	Ile	Lys	Tyr	Tyr	Pro	100	105	110	
Glu	Gln	Glu	Pro	Gln	Leu	Leu	Ser	Gly	Ile	Gly	Arg	Ile	Ser	Leu	Gln	115	120	125	
Ile	Gly	Asp	Ile	Lys	Thr	Ala	Glu	Lys	Tyr	Phe	Gln	Asp	Val	Glu	Lys	130	135	140	
Val	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Gln	Gly	Lys	Ile	Met	Val	Leu	Met	145	150	155	160
Asn	Ser	Ala	Phe	Leu	His	Leu	Gly	Gln	Asn	Asn	Phe	Ala	Glu	Ala	His	165	170	175	
Arg	Phe	Phe	Thr	Glu	Ile	Leu	Arg	Met	Asp	Pro	Arg	Asn	Ala	Val	Ala	180	185	190	
Asn	Asn	Asn	Ala	Ala	Val	Cys	Leu	Leu	Tyr	Leu	Gly	Lys	Leu	Lys	Asp	195	200	205	
Ser	Leu	Arg	Gln	Leu	Glu	Ala	Met	Val	Gln	Gln	Asp	Pro	Arg	His	Tyr	210	215	220	
Leu	His	Glu	Ser	Val	Leu	Phe	Asn	Leu	Thr	Thr	Met	Tyr	Glu	Leu	Glu	225	230	235	240
Ser	Ser	Arg	Ser	Met	Gln	Lys	Lys	Gln	Ala	Leu	Leu	Glu	Ala	Val	Ala	245	250	255	
Gly	Lys	Glu	Gly	Asp	Ser	Phe	Asn	Thr	Gln	Cys	Leu	Lys	Leu	Ala		260	265	270	

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TATAAAGAGT GACTCTCCTA TGAAGGTAAA GGCCACCCCT CTTCACTTCC AGTGACTGAG	60
ATACATTTTT CCAATCCTGG GGGCAAATAC AGACACAGCA AGTTCCTTCT TCCCTTTGGA	120
AATTTGGCAG CTGCCTTCAC CAGTGAGCAC AAAGCCACAT TTCAAAGGAA ACTGACAAAT	180
TATCCCCAGC TGCCAGAAGA AGAAATCCTC ACTGGACGGC TTCCTGTTTC CTGTGGTTCA	240
TTATCTGATT GGCTGCAGGG ATGAAAGTTT TTAAGTTCAT AGGACTGATG ATCCTCCTCA	300
CCTCTGCGTT TTCAGCCGGT TCAGGACAAA GTCCAATGAC TGTGCTGTGC TCCATAGACT	360
GGTTCATGGT CACAGTGCAC CCCTTCATGC TAAACAACGA TGTGTGTGTA CACTTTCATG	420
AACTACACTT GGGCCTGGGT TGCCCCCAA ACCATGTTCA GCCACACGCC TACCAGTTCA	480
CCTACCGTGT TACTGAATGT GGCATCAGGG CCAAAGCTGT CTCTCAGGAC ATGGTTATCT	540
ACAGCACTGA GATACACTAC TCTTCTAAGG GCACGCCATC TAAGTTTGTG ATCCCAGTGT	600
CATGTGCTGC CCCCCAAAAG TCCCCATGGC TCACCAAGCC CTGCTCCATG AGAGTAGCCA	660
GCAAGAGCAG GGCCACAGCC CAGAAGGATG AGAAATGCTA CGAGGTGTTC AGCTTGTAC	720
AGTCCAGTCA AAGGCCCAAC TGCGATTGTC CACCTTGTGT CTTCACTGAA GAAGAGCATA	780
CCCAGGTCCC TTGTCACCAA GCAGGGGCTC AGGAGGCTCA ACCTCTGCAG CCATCTCACT	840
TTCTTGATAT TTCTGAGGAT TGGTCTCTTC ACACAGATGA TATGATTGGG TCCATGTGAT	900
CCTCAGGTTT GGGGTCTCCT GAAGATGCTA TTTCTAGAAT TAGTATATAG TGTACAAATG	960
TCTGACAAAT AAGTGCTCTT GTGACCCTCA TGTGAGCACT TTTGAGAAAG AGAAACCTAT	1020
AGCAACTTCA TGAATTAAGC CTTTTTCTAT ATTTTATAT TCATGTGTAA ACAAAAAATA	1080
AAATAAAATT CTGATCGCAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1140
AAAAAAAAAA AAA	1153

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

Met Lys Val Phe Lys Phe Ile Gly Leu Met Ile Leu Leu Thr Ser Ala
1           5           10           15

Phe Ser Ala Gly Ser Gly Gln Ser Pro Met Thr Val Leu Cys Ser Ile
          20           25           30

Asp Trp Phe Met Val Thr Val His Pro Phe Met Leu Asn Asn Asp Val
          35           40           45

Cys Val His Phe His Glu Leu His Leu Gly Leu Gly Cys Pro Pro Asn
          50           55           60

His Val Gln Pro His Ala Tyr Gln Phe Thr Tyr Arg Val Thr Glu Cys
65           70           75           80

Gly Ile Arg Ala Lys Ala Val Ser Gln Asp Met Val Ile Tyr Ser Thr
          85           90           95

Glu Ile His Tyr Ser Ser Lys Gly Thr Pro Ser Lys Phe Val Ile Pro
          100          105          110

Val Ser Cys Ala Ala Pro Gln Lys Ser Pro Trp Leu Thr Lys Pro Cys
          115          120          125

Ser Met Arg Val Ala Ser Lys Ser Arg Ala Thr Ala Gln Lys Asp Glu
          130          135          140

Lys Cys Tyr Glu Val Phe Ser Leu Ser Gln Ser Ser Gln Arg Pro Asn
145          150          155          160

Cys Asp Cys Pro Pro Cys Val Phe Ser Glu Glu Glu His Thr Gln Val
          165          170          175

Pro Cys His Gln Ala Gly Ala Gln Glu Ala Gln Pro Leu Gln Pro Ser
          180          185          190

His Phe Leu Asp Ile Ser Glu Asp Trp Ser Leu His Thr Asp Asp Met
          195          200          205

Ile Gly Ser Met
          210

```

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4285 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTAATCTGT GTCTCCAGCA TTTATTTTTT TGTTTGTC ATCGGGTTCC TGGTTTTCTT	60
TTAAGACATA GTCAACTGTG TGGACCTGTA GGTTTGGGGC AGCAACCAAT TCCATTGTTT	120
TCCTTTTTGT CAAATCCAAG AGAAAATATA CCATAAGGAG CTAGAAGATT CTAGTTCACA	180
GCCTTTTGAA TCTTCATGGC CTTTGAATCC TCATGGCCTC TGAAATCTGA ATCAGTTTTTC	240
TCCCAGGARG TCTCTGGGGG CTGAGCTGCT ACAGGGGCGAR ARGGTGGGGT GGGGTGGGT	300
GGGARAATCA TCCTGGCACT TCATCGTGCA TGCTATTTTCG GGCAGCATCT TTTTTTTTTT	360
ATTTTATTAT TATTTTTTTTTT CCTGATGCTT GAGTTATGAA TGAGGATGAC CTCTGCAATC	420
ATGATGTCTC CCATAGACTC TGTTCCCTGT TCCTTTGCCA GCTTTCATCAT GCATGGTCCT	480
AACACTTCCA TGATTTAATC TGCTGCAGGA CCATAGTCTT CAGCCACCTC AGCAATAACT	540
TGTTAGAACA TTAAGGAA GTAAATTGAG AACAACTTGT TGCCATCCCA TTTTCATTAG	600
AAATCAGACA TCTTAGAGAT GTCAAGAAAG CAGCTAGCAG CTAGGGGGTA TGGGGACCTG	660
TCCTGCTCAC ACTGCTGTGT GTCAGACCAG ACCTGATCCT GGAGCTCAGG ACCCTAGAGA	720
GCCCTGATCT CTGGAACCTT TGCCACGTTG TTGCTGAGGC AGCTGAAGTC CCCATCTCCC	780
ACCATAACAA TCACAAATAG ACAGTAGTGG AGCCAGCATC CCCAGGCCCC TTTTGTGTA	840
AGCAGAAAGG GAGCTGTGAG CCTTGCCCTG TTTGCAGGTG TCAAGTGCCT CTCCCTGCCT	900
GTACTTCTCC CCTTCCTCTG AGCAGAGCTT TGGTAGCTGT TGCCAATGCA AAGAAATGTA	960
AAGCAGCAAA AGAAGACAGC AGGTTCGAC CTGAGGAGGG AAACCAAAT TATCCCACAA	1020
AGGCCCATTA ACCCCACCCC CCTCGCCTCC CACCCCAGA CTGGATCCAC TACTGGCCCA	1080
AGAATACTGA TGAGAAACCT AGTCTGGATT GGGTCGGAAG CTGGAATTTG GTGCTCTGCA	1140
GACCAGTGCT CAAAATTGTG GTTATTTTTG AGGACTCGCC TTCAATCCAG AACATTTGCG	1200
TTTCACCTTC CTCGCCCAGA TCCAGTTAAC AAGGTAGCTC ATCACTTCTT GCATCTGTTG	1260
AGTGACATGC TGGATTTTAA TTTTATTGT GGTGTACTT GGATGCAAGG AATATGTTTT	1320
GTTCTCCCA ATTTAGCGCA CCATCCTGGG AAGTGCATGT CTCAGACCAA CTCCACCTTC	1380
ACCTTACCA CCTGTGCGAT CCTGCATCCT TCAGATGAGC TCACTCGGGT CACACCAAGC	1440
CTTAACTCAG CCCCAACTCC AGCTTGTGGC AGCACCAGCC ACTTGAAATC CACGCCGGTG	1500

GCCACACCAT GCACTCCACG GAGACTGAGC CTGGCTGAGT CCTTCACTAA CACCCGTGAG 1560
TCCACGACCA CCATGAGCAC ATCCCTGGGG CTCGTGTGGC TGTGAAGGA GCGGGGCATT 1620
TCTGCTGCCG TGTACGACCC CCAGAGCTGG GACAGGGCCG GCCGGGGCTC CCTCCTGCAC 1680
TCCTACACGC CCAAGATGGC TGTGATCCCC TCTACTCCGC CGAACTCGCC TATGCAGACA 1740
CCCACATCCT CCCACCCCTC CTTTGAGTTC AAGTGCACGA GCCCTCCCTA CGACAATTTTC 1800
CTGGCTTCCA AGCCAGCCAG CTCCATCCTG AGGGAAGTGA GAGAAAAGAA CGTCCGCAGC 1860
AGCGAGAGCC AGACCGACGT GTCCGTCTCC AACCTCAACC TCGTGGACAA AGTCAGGAGG 1920
TTTGGGGTGG CCAAAGTGGT GAACTCAGGG CGAGCCCATG TCCCCACCTT GACTGAGGAG 1980
CAGGGACCCC TCCTCTGTGG GCCCCCGGGG CCAGCACCAG CCCTTGTTCC CAGAGGCCTG 2040
GTACCTGAGG GCCTGCCCCT CAGATGCCCC ACTGTCACCA GTGCCATCGG TGGGCTGCAG 2100
CTCAATAGTG GCATCCGGCG GAATCGCAGC TTCCCCACCA TGGTGGGATC TAGCATGCAG 2160
ATGAAAGCTC CTGTGACTCT CACCTCGGGC ATCTTGATGG GTGCTAAGCT CTCCAAACAA 2220
ACTAGCTTAC GGTGAGGACT GGAGGGGGGC CGGTTGCCCT AGAGGAGACC CACGTTCTCT 2280
CTTGCTCCCA CCTCCCTCTC TTCCCCCAC AGTGCCTCC CTCCCTCTGC CCTTCTCTGT 2340
CCACCCCTC CTAAGCTAGA CAAATCAACC TTGTGCCTAA TGGAGGAAGT GTGGAAACTT 2400
TGTAATGT GTACATAGGA CTTGGAGACC TTGTGTCCGC CTGCTCTTT CTTCCGATCC 2460
CACAGGAAGT GCCCTGCAC TGTCATCACT CTCACGAGGA CGTCACCTGT GCTAACCTGG 2520
GGGAAGGTGG GGTCTTTCT TCTTTCCTTT TGAGAAGCAC TGAAACTCCC AAGTGTGTTC 2580
TTATCCCATG GATAGGAAAC CAGTGAATTC CGTGGCTGGC ACACCACGAG CTGTCATGCG 2640
GCACGGGTCA TAACACATCT GGGTGTATC GGACACCTCA CCTCGCCAC CCTGTAGGAG 2700
CGTAAGGAGC CTCCATCCTC AGCCACGTGC AGCTGACGTG GCTTTCCTGA TCGGAGGGCT 2760
TTTCTTTTAT GGGTGGCCCA GCTTCTTCAA GACCTTCACT GCTCTGCCTC AGTGGACAGT 2820
CGTTTCTTTT TTGAGGTGTG ACCTTTTGTT TTCATGCCTT CCCCTTGAAG TCATCCTGTG 2880
TTTTGTAATC AGCTGTCAGG CCAAATGTCT GACCCGAAAG AGAATGTATT TACACTCATG 2940
CTGCGTTGTT CAGCAGCCCC TCTGTGTTCT GTGTGATTG TTTTATTTTT CCTTTTTTTT 3000
ACATATATAT GCAGGGAAGT AATGGTACTG GTAGTGTATG TTTTCTATGT GGTCAAATA 3060
TGAATTTTGA ACACACCAAG CCGCTAATGA GATAGCAGCT TTTTCTGGG ACCCAGAGTC 3120
ACAACCAAAT TGATTTAAGA CCGGACCCAA GACACCTTTA ACAATAGGAC TGAAAGGAAA 3180
AAGGATAGGG AAAAAGCTTA TTAAAGAAAT GTGTCAACAC CAAATGTAGA GGGGAAGAAC 3240

CACAACCAGG CATAATACCA AACCGGTTCC AGGGGGGAAAC AAGGCTTTGG TATTCCGCTG 3300
GCTCCAGCGC TTTTCTGAA ACCCGAGGCT GGCCAGGGTG CTGTCACCGT GTGGTCTTTG 3360
ATTGCAGCCA TTCAATGCCC ACATGCTTTT CCTTCTTGTT TCAGAACAGC ACATGGTCAC 3420
AACAAGATAT TTTCTTTCCC TCCAAAGCCT TTTGTCTCCT TGTGCCTCTT TTTATCCTTA 3480
GGAAAAGATC CAGGTGCTTG TGAAAAGAAT CATGAATGCA ACAAGGGAGG CTGGTCCTGT 3540
TGCTGTGCGC GATTAAGTTT TAAACTTTTA TTTATTATTT ATGTCTGCCG TATTTTAAAT 3600
AAACATTCTC GTTCCTTCCA GTTCAGTCA TAGTGTGTCT GTGGCATTCC AGTCCAACCA 3660
TGTGACTTAT TTATTCTAAT TTGAGGGCTG CACTGTACAC CATGGTGTCC TGTGACACCG 3720
TGTTCCAGAC ATTTATGGAA GGAAAACATC CCATATAAAT GAAACTGTCA TGCTGTGTCC 3780
TCCCCGGCAG CAGAAGATGT GTCCTTCCAT TGAGTGAGGG TAACCTTATG TCCACCAAGG 3840
ATACTTTGAG AAAGCCCCTA AGGAACAAGC CTCAGTCCCA CGGTTTCAGA CTATTTATTC 3900
TCTGAACACA AGAGTATTGG TTAATTATGT TCTCAGCTCT CCCTGCTGTT GTATGTGTGC 3960
ATTCACTGCA AGTAACTTAT ATCTTTTTAT TTGAATGTAT TTTAAAGCAG TAGATAGAAT 4020
AACAAAGGAA TATGAAAACC ATGGACTGAA TGGACCATT TATGTATTCA GAGAGAGAAG 4080
CCACTCATCA TTGCCAGAAA TACCATGTAA AAATTGGCAG TTCAGAGGTT GCAATACTTA 4140
GTATAGTAAA TAAATAAACG GTCAACATTG TGCAACCACT ACCAAAAAGT GTGTTGTAAT 4200
GCATCAAAAA TCAACACAAT TTTATTCAT AATGAGTATC AATAAAATAA GTTCAAATGA 4260
TGGAAACCAC AAAAAAAAAA AAAAA 4285

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Met Gln Arg Asn Val Lys Gln Gln Lys Lys Thr Ala Gly Ser Asp Leu
1 5 10 15
Arg Arg Glu Thr Lys Phe Ile Pro Gln Arg Pro Ile Asn Pro Thr Pro
20 25 30
Leu Ala Ser His Pro Gln Thr Gly Ser Thr Thr Gly Pro Arg Ile Leu

35					40					45					
Met	Arg	Asn	Leu	Val	Trp	Ile	Gly	Ser	Glu	Ala	Gly	Ile	Trp	Cys	Ser
50					55					60					
Ala	Asp	Gln	Cys	Ser	Lys	Leu	Trp	Leu	Phe	Leu	Arg	Thr	Arg	Leu	Gln
65					70					75					80
Ser	Arg	Thr	Phe	Ala	Phe	His	Leu	Pro	Arg	Pro	Asp	Pro	Val	Asn	Lys
				85					90					95	
Val	Ala	His	His	Phe	Leu	His	Leu	Leu	Ser	Asp	Met	Leu	Asp	Phe	Asn
			100					105					110		
Phe	Tyr	Cys	Gly	Cys	Thr	Trp	Met	Gln	Gly	Ile	Cys	Phe	Val	Pro	Pro
		115					120					125			
Asn	Leu	Ala	His	His	Pro	Gly	Lys	Cys	Met	Ser	Gln	Thr	Asn	Ser	Thr
						135					140				
Phe	Thr	Phe	Thr	Thr	Cys	Arg	Ile	Leu	His	Pro	Ser	Asp	Glu	Leu	Thr
145					150					155					160
Arg	Val	Thr	Pro	Ser	Leu	Asn	Ser	Ala	Pro	Thr	Pro	Ala	Cys	Gly	Ser
				165					170					175	
Thr	Ser	His	Leu	Lys	Ser	Thr	Pro	Val	Ala	Thr	Pro	Cys	Thr	Pro	Arg
			180					185					190		
Arg	Leu	Ser	Leu	Ala	Glu	Ser	Phe	Thr	Asn	Thr	Arg	Glu	Ser	Thr	Thr
		195					200					205			
Thr	Met	Ser	Thr	Ser	Leu	Gly	Leu	Val	Trp	Leu	Leu	Lys	Glu	Arg	Gly
						215						220			
Ile	Ser	Ala	Ala	Val	Tyr	Asp	Pro	Gln	Ser	Trp	Asp	Arg	Ala	Gly	Arg
225					230					235					240
Gly	Ser	Leu	Leu	His	Ser	Tyr	Thr	Pro	Lys	Met	Ala	Val	Ile	Pro	Ser
				245					250					255	
Thr	Pro	Pro	Asn	Ser	Pro	Met	Gln	Thr	Pro	Thr	Ser	Ser	Pro	Pro	Ser
			260					265					270		
Phe	Glu	Phe	Lys	Cys	Thr	Ser	Pro	Pro	Tyr	Asp	Asn	Phe	Leu	Ala	Ser
			275				280					285			
Lys	Pro	Ala	Ser	Ser	Ile	Leu	Arg	Glu	Val	Arg	Glu	Lys	Asn	Val	Arg
						295					300				
Ser	Ser	Glu	Ser	Gln	Thr	Asp	Val	Ser	Val	Ser	Asn	Leu	Asn	Leu	Val
305					310					315					320
Asp	Lys	Val	Arg	Arg	Phe	Gly	Val	Ala	Lys	Val	Val	Asn	Ser	Gly	Arg
				325					330					335	
Ala	His	Val	Pro	Thr	Leu	Thr	Glu	Glu	Gln	Gly	Pro	Leu	Leu	Cys	Gly

340	345	350
Pro Pro Gly Pro Ala Pro Ala	Leu Val Pro Arg Gly Leu Val Pro Glu	
355	360	365
Gly Leu Pro Leu Arg Cys Pro Thr Val Thr Ser Ala Ile Gly Gly Leu		
370	375	380
Gln Leu Asn Ser Gly Ile Arg Arg Asn Arg Ser Phe Pro Thr Met Val		
385	390	395
Gly Ser Ser Met Gln Met Lys Ala Pro Val Thr Leu Thr Ser Gly Ile		
405	410	415
Leu Met Gly Ala Lys Leu Ser Lys Gln Thr Ser Leu Arg		
420	425	

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

ACTTTGAATT TTTTATTTGT GAAATTAAAA ATATGGTATT ATATATATAT AACTTCTAT	60
TCCTCTATAA ATATAGATGA TTTTGTGATA GTGAACAGAA TAAATGTATA CCAAATTCAA	120
AGACCAATAT CATTTTAGCG TATGACAGAC ATAGATAAAT TTAGGTCCTA AGTACCGGCA	180
TTTTGATAAA TTCTTAAAGT TTAAAACAAT ACAATCAGGA GGATTGCTTT TCTCCTCTTC	240
TTCACAGAGA ACTAAAGTGA ATATTTTAA ATGGCTTTGA AAGATTTACA TTTGACACAT	300
TTCTGTAAAT CAAAAGAGG AGCACACAGG GATTTAATGC AGTAGACCTG CACACATTTT	360
CCCTTTAGCA TGCATGCCA TATTTTGTTT ATTTCAAGGCG CTATCTCCCC GTCAATTATT	420
CCACCTTCTT TACCTCCTGA AATCTTACCA GGTATTATT GGTGGTGTGA ATTGTTCCCC	480
CCTCAGAATG TGCTGCTGAA TAATAATCGT AATAAAATGT TGAAAGTGTA CAACTTTTAC	540
ATTTTAAAGT TTCTGATATA TGTCTAGTTA TTTGATTAAA AATAAGAAAA TAGCACTTCA	600
TTTTGAGGAA GTCCATGACA CTGAAATATC CTTCAAGTTT TCAATTTCTG TTTACGTTTT	660
GCTGTCTTGT TAAGGAAAGC AAACATCAAC TCCTTAACAA AGCTTCCAG GTGACCTCAA	720
CATTTCCATT TTACAGACCG GTAAAATCTA AGCGCAGGCT GTCTCATTCT CAAAGGCAAG	780
GTTGCCAGGC ATCCGTATGC AATTAGAATT AACATTTTAT AACCCATATC TTCAGTCTCT	840

TCCAACCCAC	ACAAAGCTTC	ATGCTTCTTC	CCAAATCTCA	GTAACCACAT	CTTTCCATGA	900
CGCTGGCCAA	ACCCATACCA	GGTTTTAGAC	ACTAGAGAAT	GAAATGAGCT	CACCCCTCAA	960
AAATTAGACT	TCAAAAAGTT	TGGCATTGGT	TATCTCACTC	ACCTGTAAAC	CAACTAAGGT	1020
GGGAGAAGGG	AGTGTCTGGC	GTTGAAGGTG	ACCGTGGAGG	GAGGCTGAGA	CTGCCAGCGC	1080
CCACACCCGT	GGGCCCCCAT	GAAGTTGGAG	GAAAGTTCTG	GACAGTTAAA	AATCCAGCTT	1140
CAGGAAGTCG	AAGGGACGGG	CCTTCGCAAT	CCACCGCCGA	GCAAGGGAGG	AATTGTAATG	1200
TATGGGGGCC	CTCCTCCAGA	TTTGGAAGGT	TTGTGGAGTT	CTGTACCTTA	AGAGCCCCTA	1260
CCTCAAGCCA	GGAAAGAAAG	GGAGGGGACA	GAAGGAGGGG	GAGGGGGCAA	AAGGAGGAGG	1320
CGGGAAGTGA	CCCTGGCAGC	GCAGCCCTAG	TCGCACCCCG	CAGTGCTGAA	CTCGCCCCGG	1380
AGCTGGCGCC	CAGCCGTCCC	GAGCACCCGT	GGTAGGGAGA	GGCGCGCGAG	GACGACCAGG	1440
AGCGCTGTGC	GGTTGCACAC	CAGTTTTAGC	TCCTTTGCAA	TACTCCGAAA	AGGGCAAGAA	1500
GAAAAGCCTC	AAATGGTTAA	ACCGCCCTAA	ATAATTAAAA	ACTTTTGAAA	AAGAAAAACG	1560
CGTGATCGGT	CGTCATTTAA	ATACAAATAT	ACTTACAAAA	ATCCTACACA	GGCTATTTAC	1620
AATCATAAAA	GCGAACAGTC	CTGGTACCAG	AGTGTGAGGG	CAAGAGGTCT	GTCCATCCTC	1680
CCTCTGGCAG	TCGGGCCCTC	GTGTCTTTTT	GCCTCAGGGA	CGGAAGCTTT	TGCAGGAGCT	1740
GAGTTGTTCT	AGGCCTCTTT	GGCCGAATTC	GGCCAAAGAG	GCCTAATTCC	TTCCTCGGTT	1800
ATTTCAATCA	GAGAATATTT	ATGAAATGCC	TACTGTGTGC	AAGTCATCCA	TCCTTGAAAA	1860
GGCCACTTCT	CAGTGAGGGA	GAGATGTAGT	GGATTCTGTG	AGACATACCT	GCTGGAGTTG	1920
AAGCAGTAAA	TAGCATGTCT	TTCCCCCTCC	CGATCTTAAG	GTGTGTTTTTC	TAGAAAAGTT	1980
CCCTAATGGA	ATTCATGAGT	TTGGGGGTCT	CAGTCACCCG	CTTGCCTGTA	GGATTCCATT	2040
TGATGATTCT	GGATTTTTGC	TGTTTGTTAT	TGCCCTTAGA	GGGGCTCTGA	GTATCTACTT	2100
GTGGGTGGCC	ATTTCTGAC	ATCTGCATGT	ACCTCGTGGA	ATTCAGCCAG	CTTCATGTTG	2160
CAAATCAGAA	AGCTGACCCC	AAGACTGCAA	ATCAATGAAG	GTATTGGCAT	TGTTAAGGTC	2220
GTAGCGTAGA	CAACAGCAGT	CATAAATAAT	TAGGCAGGAA	CTTAACCCAA	ATCTAGTTCT	2280
TTGACCACCT	CTACCACCAG	AACCCAGCAG	ACACTCACAT	CTCCTGATAA	GAGTTGCTGG	2340
ACTCGATGTT	TTTGTTTTGC	ATTTTCTCCT	CTCCTTCCCC	ACTTACTCAG	AGAATTTAAA	2400
GTCTGTAGAG	TCAGCACAGC	CCCATCAGTC	CAGGAACTTC	CCACCACCAG	CCCTTGACTG	2460
TCCCATTAAC	TGACATGGTC	AGATTTCCAG	CTCCCCCTAC	TCCCTGCTGT	GAAACAATCC	2520

CTCTCCYTGT GAGAGGAAAY TGC GCGSGAA GGYTAAGGGA GTGTGGCGGG CGGYTCCGGG	2580
AGCCAACATG CCTCGGTATG CGCAGCTGKT CATGGSCCCC GCGGGCAGCG GGAAGAGCAC	2640
Y TACTGTGCC ACCATGGTCC AGCACTGTGA AGCCYTCAAC CGGTCTGTCC AAGTTGTAAA	2700
CCTGGATCCA GCAGCAGAAC ACTTCAAYTA CTCCGTGATG GCTGACATCC GGGAACTGAT	2760
CGAGGTGGAT GATGTAATGG AGGATGATTY TYTGCGATTC GGTCCCAACG GAGGATTGGT	2820
ATTTTGCATG GAGTACTTTG CCAATAATTT T GACTGGCTG GAGAACTGTC TTGGCCATGT	2880
AGAGGACGAC TATATCCTTT TTGATTGTCC AGGTCAGATT GAGTTGTACA CTCACCTGCC	2940
TGTGATGAAA CAGCTGGTCC AGCAGCTCGA GCAGTGGGAG TTCCGAGTCT GTGGAKTTTY	3000
TYTTGTTGAT TCTCAGTTCA TGGTGGAGTC ATTCAAGTTT ATTTCTGGCA TCTTGGCAGC	3060
CCTGAGTGCC ATGATCTCTC TAGAAATTCC GCAAGTCAAC ATCATGACAA AAATGGATCT	3120
GCTGAGTAAA AAAGCAAAAA AGGAAATTGA GAAATTTTTA GATCCAGACA TGTATTCTTT	3180
ATTAGAAGAT TCTACAAGTG ACTTAAGAAG CAAAAAATTC AAGAACTGA CTAAAGCTAT	3240
ATGTGGACTG ATTGATGACT ACAGCATGGT TCGATTTTTA CCTTACGATC AGTCAGATGA	3300
AGAAAGCATG AACATTGTAT TGCAGCATAT TGATTTTGCC ATTCAATATG GAGAAGACCT	3360
AGAATTTAAA GAACCAAAGG AACGTGAAGA TGAGTCTTCC TCTATGTTTG ACGAATATTT	3420
TCAAGAATGC CAGGATGAAT GAAGAGTTTA CTAAAAGTAA CCATCTAAAG AGCTTGTTGC	3480
CAAACCAGCA GAACATTCTT CTYTTCAAAG GATGCAATAG TAGAAAGCTA CTTATTTTAA	3540
TGAAAAAAG TAAAACTTCG TTCTTTATCA GCCTCATGCC TGAATCAAAT TTTTAATTAT	3600
TCTGAAACTG CTGCTGTTTA AAGTGAATC TTTTAGTATT ATAACAGCAT CACTTTAGAT	3660
TTTGTAAGTC AAAATTGAAA TGAATGCACA TAGATTTATA TATAAATTAG CACCTGAGCT	3720
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA A	3751

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Met Pro Arg Tyr Ala Gln Leu Xaa Met Xaa Pro Ala Gly Ser Gly Lys

1	5	10	15
Ser Thr Tyr Cys Ala Thr Met Val Gln His Cys Glu Ala Xaa Asn Arg	20	25	30
Ser Val Gln Val Val Asn Leu Asp Pro Ala Ala Glu His Phe Asn Tyr	35	40	45
Ser Val Met Ala Asp Ile Arg Glu Leu Ile Glu Val Asp Asp Val Met	50	55	60
Glu Asp Asp Xaa Leu Arg Phe Gly Pro Asn Gly Gly Leu Val Phe Cys	65	70	75
Met Glu Tyr Phe Ala Asn Asn Phe Asp Trp Leu Glu Asn Cys Leu Gly	85	90	95
His Val Glu Asp Asp Tyr Ile Leu Phe Asp Cys Pro Gly Gln Ile Glu	100	105	110
Leu Tyr Thr His Leu Pro Val Met Lys Gln Leu Val Gln Gln Leu Glu	115	120	125
Gln Trp Glu Phe Arg Val Cys Gly Xaa Xaa Xaa Val Asp Ser Gln Phe	130	135	140
Met Val Glu Ser Phe Lys Phe Ile Ser Gly Ile Leu Ala Ala Leu Ser	145	150	155
Ala Met Ile Ser Leu Glu Ile Pro Gln Val Asn Ile Met Thr Lys Met	165	170	175
Asp Leu Leu Ser Lys Lys Ala Lys Lys Glu Ile Glu Lys Phe Leu Asp	180	185	190
Pro Asp Met Tyr Ser Leu Leu Glu Asp Ser Thr Ser Asp Leu Arg Ser	195	200	205
Lys Lys Phe Lys Lys Leu Thr Lys Ala Ile Cys Gly Leu Ile Asp Asp	210	215	220
Tyr Ser Met Val Arg Phe Leu Pro Tyr Asp Gln Ser Asp Glu Glu Ser	225	230	235
Met Asn Ile Val Leu Gln His Ile Asp Phe Ala Ile Gln Tyr Gly Glu	245	250	255
Asp Leu Glu Phe Lys Glu Pro Lys Glu Arg Glu Asp Glu Ser Ser Ser	260	265	270
Met Phe Asp Glu Tyr Phe Gln Glu Cys Gln Asp Glu	275	280	

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TNCAGGCCTT GCGTTCCTAG CTGCTCTGC

29

- (2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GNGCTGTGAG TTTATCCACA AAGGAACAG

29

- (2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GNATAGGAGG TCCCAAGTTA TCAAGGTTT

29

- (2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GNTTTCCTGG TTCTTGGTCA GGTTCCTC

29

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CNAGATGCAA TGGTTGTGAG ATTGACCAA

29

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GNCACTTCC ACTGCTGTGA GCTTGTCAT

29

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ANCAGACAGT TTGCCATGGA GTACATCAC

29

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TNATGAACCA CAGGAAACAG GAAGCCGTC

29

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TNAAGGTGAA GGTGGAGTTG GTCTGAGAC

29

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GNCAGAAATA AACTTGAATG ACTCCACCA

29

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS :

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Asn Ser Gln Leu Asn Ser Phe Thr Gly Gln Met Glu Asn Ile Thr
1 5 10 15

Thr Ile Ser Gln Ala Asn Glu Gln Asn Leu Lys Asp Leu Gln Asp Leu
20 25 30

His Lys Asp Ala Glu Asn Arg Thr Ala Ile Lys Phe Asn Gln Leu Glu
35 40 45

Glu Arg Phe Gln Leu Phe Glu Thr Asp Ile Val Asn Ile Ile Ser Asn
50 55 60

Ile Ser Tyr Thr Ala His His Leu Arg Thr Leu Thr Ser Asn Leu Asn
65 70 75 80

Glu Val Arg Thr Thr Cys Thr Asp Thr Leu Thr Lys His Thr Asp Asp
85 90 95

Leu Thr Ser Leu Asn Asn Thr Leu Ala Asn Ile Arg Leu Asp Ser Val
100 105 110

Ser Leu Arg Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu
115 120 125

Val Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser
130 135 140

Lys His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro
145 150 155 160

Gly Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly
165 170 175

Pro Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro
180 185 190

Pro Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro
195 200 205

Gly Glu Arg Gly Gly Lys Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly
210 215 220

Ser Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp
225 230 235 240

Pro Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln
245 250 255

Gly Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly
260 265 270

Val Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met
275 280 285

Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Ala Val
290 295 300

Val Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn
305 310 315 320

Ser Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe
325 330 335

Ser Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp
340 345 350

Lys Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp
355 360 365

Ile Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr
370 375 380

Asp Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro
385 390 395 400

Asp Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly
405 410 415

His Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp
420 425 430

Asn Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp
435 440 445

Arg Glu Thr Val Leu Ser Ser Ala Leu
450 455

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Cys Gly His His Glu Leu Asn Asn Leu Asn Leu Thr Gln Val Gln Gln
1 5 10 15

Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val Asp Asp Thr Ser Gln
20 25 30

Ala Ile Gln Arg Ile Lys Asn Asp Phe Gln Asn Leu Gln Gln Val Phe
35 40 45

Leu Gln Ala Lys Lys Asp Thr Asp Trp Leu Lys Glu Lys Val Gln Ser
50 55 60

Leu Gln Thr Leu Ala Ala Asn Asn Ser Ala Leu Ala Lys Ala Asn Asn
65 70 75 80

Asp Thr Leu Glu Asp Met Asn Ser Gln Leu Asn Ser Phe Thr Gly Gln
85 90 95

Met Glu Asn Ile Thr Thr Ile Ser Gln Ala Asn Glu Gln Asn Leu Lys
100 105 110

Asp Leu Gln Asp Leu His Lys Asp Ala Glu Asn Arg Thr Ala Ile Lys
115 120 125

Phe Asn Gln Leu Glu Glu Arg Phe Gln Leu Phe Glu Thr Asp Ile Val
130 135 140

Asn Ile Ile Ser Asn Ile Ser Tyr Thr Ala His His Leu Arg Thr Leu
145 150 155 160

Thr Ser Asn Leu Asn Glu Val Arg Thr Thr Cys Thr Asp Thr Leu Thr
165 170 175

Lys His Thr Asp Asp Leu Thr Ser Leu Asn Asn Thr Leu Ala Asn Ile
180 185 190

Arg Leu Asp Ser Val Ser Leu Arg Met Gln Gln Asp Leu Met Arg Ser
195 200 205

Arg Leu Asp Thr Glu Val Ala Asn Leu Ser Val Ile Met Glu Glu Met
210 215 220

Lys Leu Val Asp Ser Lys His Gly Gln Leu Ile Lys Asn Phe Thr Ile
225 230 235 240

Leu Gln Gly Pro Pro Gly Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser
245 250 255

Gln Gly Pro Pro Gly Pro Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys
260 265 270

Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly
275 280 285

Pro Ala Gly Pro Pro Gly Glu Arg Gly Gly Lys Gly Ser Lys Gly Ser
290 295 300

Gln Gly Pro Lys Gly Ser Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln
305 310 315 320

Gly Pro Ser Gly Asp Pro Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly
325 330 335

Leu Pro Gly *Pro Gln Gly Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr
 340 345 350
 Val Gly Glu Pro Gly Val Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro
 355 360 365
 Gly Val Pro Gly Met Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly
 370 375 380
 Pro Ser Gly Ala Val Val Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro
 385 390 395 400
 Ala Pro Glu Asp Asn Ser Cys Pro Pro His Trp Lys Asn Phe Thr Asp
 405 410 415
 Lys Cys Tyr Tyr Phe Ser Val Glu Lys Glu Ile Phe Glu Asp Ala Lys
 420 425 430
 Leu Phe Cys Glu Asp Lys Ser Ser His Leu Val Phe Ile Asn Thr Arg
 435 440 445
 Glu Glu Gln Gln Trp Ile Lys Lys Gln Met Val Gly Arg Glu Ser His
 450 455 460
 Trp Ile Gly Leu Thr Asp Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu
 465 470 475 480
 Asp Gly Thr Ser Pro Asp Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp
 485 490 495
 Asn Trp Gly His Gly His Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile
 500 505 510
 Tyr Ala Gly Gln Trp Asn Asp Phe Gln Cys Glu Asp Val Asn Asn Phe
 515 520 525
 Ile Cys Glu Lys Asp Arg Glu Thr Val Leu Ser Ser Ala Leu
 530 535 540